

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:54:28 ; Search time 2925.11 Seconds  
(without alignments)  
7749.596 Million cell updates/sec

Title: US-09-733-368A-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgtccctctgtgtgtt.....accacattgtgtgacctc 523

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1:	gb_pa.*	GenEmbl.*
2:	gb_htg.*	
3:	gb_in.*	
4:	gb_om.*	
5:	gb_ov.*	
6:	gb_pat.*	
7:	gb_ph.*	
8:	gb_pl.*	
9:	gb_pr.*	
10:	gb_ro.*	
11:	gb_sts.*	
12:	gb_sy.*	
13:	gb_un.*	
14:	gb_vi.*	
15:	em_ba.*	
16:	em_fun.*	
17:	em_hum.*	
18:	em_in.*	
19:	em_mu.*	
20:	em_om.*	
21:	em_or.*	
22:	em_ov.*	
23:	em_pat.*	
24:	em_ph.*	
25:	em_pl.*	
26:	em_ro.*	
27:	em_sts.*	
28:	em_un.*	
29:	em_vi.*	
30:	em_htg_hum.*	
31:	em_htg_inv.*	
32:	em_htg_other.*	
33:	em_htg_mus.*	
34:	em_htg_pin.*	
35:	em_htg_rod.*	
36:	em_htg_mam.*	
37:	em_htg_vrt.*	
38:	em_sy.*	
39:	em_htgo_hum.*	
40:	em_htgo_mus.*	
41:	em_htgo_other.*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	523	100.0	648	6	AX175190	AX175190 Sequence
2	523	100.0	648	6	AX175195	AX175195 Sequence
3	519.8	99.4	7086	6	AX743955	AX743955 Sequence
4	517.8	99.0	2245	6	AX643582	AX643582 Sequence
5	517.8	99.0	6289	12	XXU42373	U42373 Cloning vec
6	515.6	98.6	3256	14	ALRDA2	L29199 Rous sarcom
7	515	98.5	4965	6	AR071323	AR071323 Sequence
8	514	98.3	1016	14	REASV3	V01167 Avian sarco
9	513.8	98.2	562	6	AX643583	AX643583 Sequence
10	508.8	97.3	4457	6	AX743954	AX743954 Sequence
11	508.8	97.3	7334	6	AX743956	AX743956 Sequence
12	505.6	96.7	3557	12	SYNRSV3MV	M83240 Cloning vec
13	505.6	96.7	4059	6	AR071324	AR071324 Sequence
14	505.6	96.7	4341	6	A38214	A38214 Sequence 58
15	505.6	96.7	4341	6	AX286570	AX286570 Sequence
16	505.6	96.7	4839	12	SYNRSV5GPT	M83236 Cloning vec
17	505.6	96.7	5108	12	SYNRSV5NEO	M83237 cDNA expres
18	505.6	96.7	5564	12	SYNTRC	L36555 Cloning vec
19	505.6	96.7	5653	6	I56772	I56772 Sequence 3
20	505.6	96.7	5653	6	I95540	I95540 Sequence 1
21	505.6	96.7	5736	12	SYNRSVNEO	M77786 pRSVneo clo
22	505.6	96.7	6864	12	XXU19931	U19931 Cloning vec
23	505.6	96.7	8591	6	I58322	I58322 Sequence 6
24	505.6	96.7	8591	6	I58323	I58323 Sequence 8
25	505.6	96.7	8591	6	I60508	I60508 Sequence 6
26	505.6	96.7	8591	6	I60509	I60509 Sequence 8
27	505.6	96.7	8591	6	I77052	I77052 Sequence 6
28	505.6	96.7	8591	6	I77053	I77053 Sequence 8
29	505.6	96.7	8591	6	I87173	I87173 Sequence 6
30	505.6	96.7	8591	6	I87174	I87174 Sequence 8
31	505.6	96.7	10737	12	XXU02428	U02428 Cloning vec
32	505.6	96.7	10850	12	U02455	U02455 Cloning vec
33	504.8	96.5	633	14	ALRPR0LTB	J02025 Rous sarcom
34	500.8	95.8	6836	6	AR215114	AR215114 Sequence
35	500.8	95.8	6836	6	AR302356	AR302356 Sequence
36	500.8	95.8	6836	6	AR373228	AR373228 Sequence
37	500.8	95.8	6836	6	AR401614	AR401614 Sequence
38	500.8	95.8	6836	12	AF346624	AF346624 RAGE vect
39	500.8	95.8	9737	6	AR215118	AR215118 Sequence
40	500.8	95.8	9737	6	AR215119	AR215119 Sequence
41	500.8	95.8	9737	6	AR215124	AR215124 Sequence
42	500.8	95.8	9737	6	AR302360	AR302360 Sequence
43	500.8	95.8	9737	6	AR302361	AR302361 Sequence
44	500.8	95.8	9737	6	AR302366	AR302366 Sequence
45	500.8	95.8	9737	6	AR373232	AR373232 Sequence
46	500.8	95.8	9737	6	AR373233	AR373233 Sequence
47	500.8	95.8	9737	6	AR373238	AR373238 Sequence
48	500.8	95.8	9737	6	AR401618	AR401618 Sequence
49	500.8	95.8	9737	6	AR401619	AR401619 Sequence
50	500.8	95.8	9737	6	AR401624	AR401624 Sequence
51	500.8	95.8	9871	6	AR215120	AR215120 Sequence
52	500.8	95.8	9871	6	AR302362	AR302362 Sequence
53	500.8	95.8	9871	6	AR373234	AR373234 Sequence
54	500.8	95.8	9871	6	AR401620	AR401620 Sequence
55	500.8	95.8	10060	6	AR215121	AR215121 Sequence
56	500.8	95.8	10060	6	AR302363	AR302363 Sequence
57	500.8	95.8	10060	6	AR373235	AR373235 Sequence
58	500.8	95.8	10060	6	AR401621	AR401621 Sequence
59	500.8	95.8	11265	6	AX031159	AX031159 Sequence
60	500.8	95.8	11265	6	BD084805	BD084805 Enhanceme
61	472	90.2	565	6	AR202606	AR202606 Sequence
62	472	90.2	565	6	BD005463	BD005463 Cellular
63	472	90.2	565	14	U41728	U41728 Rous sarcom
64	470.6	90.0	9317	14	ALRSPDCG	D10652 Rous sarcom
65	468.8	89.6	5647	12	CVU64449	U64449 Cloning vec

Db	150	ACACGCCAAGGCTTGACCGCAAAATTCGATGAGAAATCGCTTAGGGTTAGGCGGTTTTCGG	209
Qy	121	CTGCTTCGCATGTACGGGCCAGATATTGCGGTATCTGACGGGCACTTAGGGTGTGTTTAGG	180
Db	210	CTGCTTCGCATGTACGGGCCAGATATTGCGGTATCTGACGGGCACTTAGGGTGTGTTTAGG	269
Qy	181	CGAAAGCGGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCG	240
Db	270	CGAAAGCGGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCG	329
Qy	241	TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACTCTTTGAGTCTTGCAACTGG	300
Db	330	TTTTCATAGGGAGGGGAAATGTAGTCTTATGCAATACTCTTTGAGTCTTGCAACTGG	389
Qy	301	TAACGATGAGTTAGCAACATCCCTTACAGGAGAGAAAGCACCGTGCATGCCGATTCGG	360
Db	390	TAACGATGAGTTAGCAACATCCCTTACAGGAGAGAAAGCACCGTGCATGCCGATTCGG	449
Qy	361	TGGAAGTAAAGTGTTAGCATCGTCCCTTATTAGGAGGCAACAGACGGGCTGCACATGGA	420
Db	450	TGGAAGTAAAGTGTTAGCATCGTCCCTTATTAGGAGGCAACAGACGGGCTGCACATGGA	509
Qy	421	TTTGACGAACCACTAAATTCGCGAATTGCAGATATTGTTATTTAAAGTGCCTTAGCTGATA	480
Db	510	TTTGAGCAACCACTAAATTCGCGAATTGCAGATATTGTTATTTAAAGTGCCTTAGCTGATA	569
Qy	481	CAATAAAGCCGCTTTGACCATTCACACATTTGGTGTGCACCTC	523
Db	570	CAATAAAGCCGCTTTGACCATTCACACATTTGGTGTGCACCTC	612

1. Rivera V, Zoltick P, and Wilson J.M.  
Methods for expression of genes in primates  
Patent: WO 0142443-A 6 14-JUN-2001;  
ARIAD GENE THERAPEUTICS, INC. (US) ; THE UNIVERSITY OF PENNSYLVANIA  
(US).

```

FEATURES
  (US)
    source
      Location/Qualifiers
        1..648
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="MluI/RSV promoter/BglII"

```

Qy	61	ACAGGGCAGGCTTGACCGACAAATGCATCAGAGATCTGCTTAGGGTTAGCGCTTTGGC	120
		150	ACAGGGCAGGCTTGACCGACAAATGCATCAGAGATCTGCTTAGGGTTAGCGCTTTGGC
Db	150	ACAGGGCAGGCTTGACCGACAAATGCATCAGAGATCTGCTTAGGGTTAGCGCTTTGGC	209
Qy	121	CTGCTTCGCGATGTACGGCCAGATATATCGCTATCTCAGGGGACTAGGCTGTGTTAGG	180
		210	CTGCTTCGCGATGTACGGCCAGATATATCGCTATCTCAGGGGACTAGGCTGTGTTAGG
Db	210	CTGCTTCGCGATGTACGGCCAGATATATCGCTATCTCAGGGGACTAGGCTGTGTTAGG	269
Qy	181	CGAAAAGCGGGGCTTCGGTTCTACCGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC	240

```

Db 270 CGAAAGCGGGCTTCGGTGTACGGGTAGAGTCCCTCAGGATATAGTAGTTTCGC 329
QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGGCAACATGG 300
Db 330 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGGCAACATGG 389
QY 301 TAACGATGATGTTAGCAACATCCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATGG 360
Db 390 TAACGATGATGTTAGCAACATCCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATGG 449
QY 361 TGGAGTAAAGTGTGATAGATGCTCTTATGAGAGGCAACAGAGGGTCTGACATGGA 420
Db 450 TGGAGTAAAGTGTGATAGATGCTCTTATGAGAGGCAACAGAGGGTCTGACATGGA 509
QY 421 TTGGAGCAACCACTAAATTCGCATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATA 480
Db 510 TTGGAGCAACCACTAAATTCGCATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATA 569
QY 481 CAATAAACGCCATTGACCACTTCAACCAATTTGGTGTGCACCTC 523
Db 570 CAATAAACGCCATTGACCACTTCAACCAATTTGGTGTGCACCTC 612

RESULT 3
AX743955/c
LOCUS AX743955 7086 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 3 from Patent WO03031630.
ACCESSION AX743955
VERSION AX743955.1 GI:30722652
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1.
AUTHORS Razio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.
TITLE Multi-clonistic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 3 17-APR-2003;
Keryos Spa (IT)
FEATURES
Location/Qualifiers
source
1..7086
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 99.4%; Score 519.8; DB 6; Length 7086;
Best Local Similarity 99.6%; Pred. No. 3.1e-147;
Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60
Db 2055 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 1996
QY 61 ACAGGCAAGGCTTACCGCAATTCATGAGATCTGCTTAGGGTTAGCGCTTTTGGC 120
Db 1995 ACAGGCAAGGCTTACCGCAATTCATGAGATCTGCTTAGGGTTAGCGCTTTTGGC 1936
QY 121 CTGCTCCGATGACGGGCCAGAAATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180
Db 1935 CTGCTCCGATGACGGGCCAGAAATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 1876
QY 181 CGAAAACGGGGCTTCGGTGTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240
Db 1875 CGAAAACGGGGCTTCGGTGTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 1816
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAACATGG 300
Db 1815 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAACATGG 1756
QY 301 TAACGATGATGTTAGCAACATCCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATGG 360
Db 1755 TAACGATGATGTTAGCAACATCCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATGG 1696

```

```

QY 361 TGGAGTAAAGTGTGATAGATGCTCTTATGAGAGGCAACAGAGGGTCTGACATGGA 420
Db 1695 TGGAGTAAAGTGTGATAGATGCTCTTATGAGAGGCAACAGAGGGTCTGACATGGA 1636
QY 421 TTGGACGCAACCACTAAATTCGCATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATA 480
Db 1635 TTGGACGCAACCACTAAATTCGCATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATA 1576
QY 481 CAATAAACGCCATTGACCACTTCAACCAATTTGGTGTGCACCTC 523
Db 1575 CAATAAACGCCATTGACCACTTCAACCAATTTGGTGTGCACCTC 1533

RESULT 4
AX643582
LOCUS AX643582 2245 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 1 from Patent WO02099100.
ACCESSION AX643582
VERSION AX643582.1 GI:28551382
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1.
AUTHORS Al-Rubeai, M. and Shuttleworth, J.
TITLE Method of production of a protein in cells which inducibly express
the cell cycle inhibitor protein, p21
JOURNAL Patent: WO 02099100-A 1 12-DEC-2002;
Lonza Biologics plc (GB)
FEATURES
Location/Qualifiers
source
1..2245
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
/notice="RSV-LTR promoter + intron + p21 cds + Tkpoly(A)
LacSwitch II expression construct"
ORIGIN
Query Match 99.0%; Score 517.8; DB 6; Length 2245;
Best Local Similarity 99.6%; Pred. No. 1.2e-146;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60
Db 46 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 105
QY 61 ACAGGCAAGGCTTACCGCAATTCATGAGATCTGCTTAGGGTTAGGGTGTGTTGGC 120
Db 106 ACAGGCAAGGCTTACCGCAATTCATGAGATCTGCTTAGGGTTAGGGTGTGTTGGC 155
QY 121 CTGCTCCGATGACGGGCCAGAAATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180
Db 166 CTGCTCCGATGACGGGCCAGAAATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 225
QY 181 CGAAAACGGGGCTTCGGTGTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240
Db 226 CGAAAACGGGGCTTCGGTGTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 285
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAACATGG 300
Db 286 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAACATGG 345
QY 301 TAAAGATGATGATAGCAACATCCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATGG 360
Db 346 TAAAGATGATGATAGCAACATCCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATGG 405
QY 361 TGGAGTAAAGTGTGATAGATGCTCTTATGAGAGGCAACAGAGGGTCTGACATGGA 420
Db 406 TGGAGTAAAGTGTGATAGATGCTCTTATGAGAGGCAACAGAGGGTCTGACATGGA 465
QY 421 TTGGACGCAACCACTAAATTCGCATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATA 480

```

```

|||||
466 TTGGACGAACCACTGAAATTCGGCATTCGACGAGATATTGATTAAAGTGCCTAGCTCGATA 525
|||||
QY 481 CAATAACGCCATTGACCAATTCACACACATTGGTGTGCACC 521
|||||
Db 526 CAATAAACGCCATTGACCAATTCACACACATTGGTGTGCACC 566
|||||

RESULT 5
XXU42373
LOCUS XXU42373 6289 bp DNA circular SYN 05-JAN-1996
DEFINITION Cloning vector pOP13Cat target vector from Lacswitch System.
ACCESSION U42373
VERSION U42373.1 GI:1147762
KEYWORDS Cloning vector pOP13Cat
SOURCE Cloning vector pOP13Cat
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 6289)
AUTHORS Marsh, S.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-1995) Sam Marsh, Marketing, Stratagene, 11011
North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES
    source
        1..6289
            /organism="Cloning vector pOP13Cat"
            /mol_type="genomic DNA"
            /db_xref="taxon:44740"
            /plasmid="pOP13Cat"

ORIGIN
Query Match 99.0%; Score 517.8; DB 12; Length 6289;
Best Local Similarity 99.6%; Pred. No. 1.3e-146;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGCTGGAGTTCGCTGAGTACGCGCGAGCAAAATTAAAGTACA 60
|||||
Db 2106 CTGCTCCCTGCTTGCTGGAGTTCGCTGAGTACGCGCGAGCAAAATTAAAGTACA 2165
|||||
QY 61 ACAAGGCAAGGCTTACCGCAATTCATGAGAGATCTGCTTAGGCTTAGCGCTTTGCG 120
|||||
Db 2166 ACAAGGCAAGGCTTACCGCAATTCATGAGAGATCTGCTTAGGCTTAGCGCTTTGCG 2225
|||||
QY 121 CTGCTTCGCATGTACGGGCGACATATCGCGTATCTGAGGGACTAGGGTGTGTTAGG 180
|||||
Db 2226 CTGCTTCGCATGTACGGGCGACATATACGCTATCTGAGGGACTAGGGTGTGTTAGG 2285
|||||
QY 181 CGAAAGCGGGCTTCGGTGTACGCGGTAGGAGTCCCTCAGGATATAGTACTTTCGC 240
|||||
Db 2286 CGAAAGCGGGCTTCGGTGTACGCGGTAGGAGTCCCTCAGGATATAGTACTTTCGC 2345
|||||
QY 241 TTTTTCATAGGGAGGGGGAATGTACTTATGCAATACTCTTGTAGTCTTGGCAACATGG 300
|||||
Db 2346 TTTTTCATAGGGAGGGGGAATGTACTTATGCAATACTCTTGTAGTCTTGGCAACATGG 2405
|||||
QY 301 TAAAGATAGTATAGCAATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 360
|||||
Db 2406 TAAAGATAGTATAGCAATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 2465
|||||
QY 361 TGGAGTATAGTGTACCATCGTCCCTTATTAGGAGGCAACAGCGGCTCTGACATGGA 420
|||||
Db 2466 TGGAGTATAGTGTACCATCGTCCCTTATTAGGAGGCAACAGCGGCTCTGACATGGA 2525
|||||
QY 421 TTGGACGAACCACTAAATTCGCATTCGACAGATATTGTTTAAAGTGCCTAGCTCGATA 480
|||||
Db 2526 TTGGACGAACCACTAAATTCGCATTCGACAGATATTGTTTAAAGTGCCTAGCTCGATA 2585
|||||
QY 481 CAATAACGCCATTGACCAATTCACACACATTGGTGTGCACC 521
|||||
Db 2586 CAATAACGCCATTGACCAATTCACACACATTGGTGTGCACC 2626
|||||

RESULT 6

```

```

ALRDA2
LOCUS Rous sarcoma virus 3256 bp DNA linear VRL 12-APR-1999
DEFINITION Rous sarcoma virus (Schmidt-Ruppin A) env-src-3'LTR.
ACCESSION L29199 J02018 J02026 J02352 K01194 K01195 N00021
VERSION L29199.1 GI:459672
KEYWORDS c-myc proto-oncogene; kinase; protein kinase; src oncogene.
SEGMENT 2 of 2
SOURCE Rous sarcoma virus
ORGANISM Rous sarcoma virus
VIRUSES; Retroid viruses; Retroviridae; Alpharetrovirus.
REFERENCE 1 (sites)
AUTHORS Czernilofsky, A.P., DeLorbe, W., Swanstrom, R., Varmus, H.E., Bishop, J.M., Fischer, E. and Goodman, H.M.
TITLE The nucleotide sequence of an untranslated but conserved domain at the 3' end of the avian sarcoma virus genome
JOURNAL Nucleic Acids Res. 8 (13), 2967-2984 (1980)
MEDLINE 81053726
PUBMED 6253899
REFERENCE 2 (sites)
AUTHORS Czernilofsky, A.P., Levinson, A.D., Varmus, H.E., Bishop, J.M., Fischer, E. and Goodman, H.M.
TITLE Nucleotide sequence of a cloned un Integrated avian sarcoma virus DNA: proposed amino acid sequence for gene product
JOURNAL Nature 287 (5779), 198-203 (1980)
MEDLINE 81052295
PUBMED 6253794
REFERENCE 3 (sites)
AUTHORS Swanstrom, R., DeLorbe, W.J., Bishop, J.M. and Varmus, H.E.
TITLE Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA: viral DNA contains direct and inverted repeats similar to those in transposable elements
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (1), 124-128 (1981)
MEDLINE 81223697
PUBMED 6264426
REFERENCE 4 (sites)
AUTHORS Swanstrom, R., Varmus, H.E. and Bishop, J.M.
TITLE Nucleotide sequence of the 5' noncoding region and part of the gag gene of Rous sarcoma virus
JOURNAL J. Virol. 41 (2), 535-541 (1982)
MEDLINE 82192582
PUBMED 6281465
REFERENCE 5 (sites)
AUTHORS Hughes, S.H.
TITLE Sequence of the long terminal repeat and adjacent segments of the endogenous avian virus Rous-associated virus 0
JOURNAL J. Virol. 43 (1), 191-200 (1982)
MEDLINE 82269131
PUBMED 6286997
REFERENCE 6 (sites)
AUTHORS Misra, T.K., Grandgenett, D.P. and Parsons, J.T.
TITLE Avian retrovirus pp32 DNA-binding protein. I. Recognition of specific sequences on retrovirus DNA terminal repeats
JOURNAL J. Virol. 44 (1), 330-343 (1982)
MEDLINE 83059884
PUBMED 6292495
REFERENCE 7 (sites)
AUTHORS Czernilofsky, A.P., Levinson, A.D., Varmus, H.E., Bishop, J.M., Fischer, E. and Goodman, H.
TITLE Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus
JOURNAL Nature 301 (5902), 736-738 (1983)
MEDLINE 83414780
PUBMED 6299633
REFERENCE 8 (sites)
AUTHORS Sorge, J., Ricci, W. and Hughes, S.H.
TITLE cis-Acting RNA packaging locus in the 11S-nucleotide direct repeat of Rous sarcoma virus
JOURNAL J. Virol. 48 (3), 667-675 (1983)
MEDLINE 84036404
PUBMED 6313966
REFERENCE 9 (sites)
AUTHORS Hughes, S. and Kosik, E.
TITLE Mutagenesis of the region between env and src of the SR-A strain of

```



Rous sarcoma virus for the purpose of constructing helper-independent vectors

Virology 136 (1), 89-99 (1984)

84251740

6330999

10 (sites)

Petersen,R.B., Hensel,C.H. and Hackett,P.B.

Identification of a ribosome-binding site for a leader peptide

encoded by Rous sarcoma virus RNA

J. Virol. 51 (3), 722-729 (1984)

84292449

6088795

11 (sites)

Hughes,S., Mellstrom,K., Kosik,E., Tamanoi,F. and Brugge,J.

Mutation of a termination codon affects src initiation

Mol. Cell. Biol. 4 (9), 1738-1746 (1984)

85036324

6092936

12 (sites)

Resnick,R., Omer,C.A. and Faras,A.J.

Involvement of retrovirus reverse transcriptase-associated RNase H

in the initiation of strong-stop (+) DNA synthesis and the

generation of the long terminal repeat

J. Virol. 51 (3), 813-821 (1984)

84292461

6206236

13 (sites)

Pellman,D., Garber,E.A., Cross,F.R. and Hanafusa,H.

Fine structural mapping of a critical NH2-terminal region of p60src

Proc. Natl. Acad. Sci. U.S.A. 82 (6), 1623-1627 (1985)

85166183

2984663

14 (sites)

Maroney,A.C., Oureshi,S.A., Foster,D.A. and Brugge,J.S.

Cloning and characterization of a thermostable v-src gene for use

in reversible transformation of mammalian cells

Oncogene 7 (6), 1207-1214 (1992)

92278773

1375718

The bases as they are found in the references are listed below:

1-3107 Nature 287, 198-203 (1980)

2907-3256 Proc. Natl. Acad. Sci. U.S.A. 78, 124-128 (1981)

2244-3176 Nucleic Acids Res. 8, 2967-2984 (1980)

700-908 J. Virol. 43, 191-200 (1982)

2927-3176 J. Virol. 44, 330-343 (1982)

1-3107 Nature 301, 736-738 (1983)

706-900 and 2791-2930 J. Virol. 48, 667-675 (1983)

721-1140 Mol. Cell. Biol. 4, 1738-1746 (1984)

2912-2938 J. Virol. 51, 813-821 (1984)

873-882 and 990-1128 Virology 136, 89-99 (1984)

1121-1173 Proc. Nat. Acad. Sci. U.S.A. 82, 1623-1627 (1985) [1]

revised by [7].

[7] revises [1].

See comment in segment 1.

The src gene is believed to have been obtained from avian DNA when

an ALV-like virus recombined with host DNA. Homology to the c-src

gene of chicken begins at position 1032. A direct repeat of about

100 bp is present near either end of exon 2 the 21S (src) mRNA.

These repeats include positions 772-899 and 2703-2799. A

polyadenylation signal is present at position 3149-3154. [7]

contains a revision of the sequence in [1]. Individual revisions

are not noted in sites.

[9] mutated the 'tga' stop codon at position 1057-1059 to 'cga' and

found that the mutant strain produced an src protein extended at

the NH-terminal end.

[10] created a synthetic Rous sarcoma virus lacking the direct

repeat 5' of src-p60 and with ClaI sites flanking src-p60 to create

a vector capable of expressing genes inserted in place of src-p60

(see RSV vector in synthetic sections).

[11] used mutants with alterations in the N-terminal region of the

src-p60 gene to determine the requirements for N-myristylation of

src-p60. The site of addition of myristic acid is the cytosine

residue at amino acid position 2 (position 1126-1128 of this

sequence).

FEATURES	Location/Qualifiers	sequence)
source	1..3256	
	/organism="Rous sarcoma virus"	
	/proviral	
	/mol_type="genomic DNA"	
	/strain="Schmidt-Ruppin A"	
	/db_xref="taxon:11886"	
mRNA	<1..3176	
	/product="35Ss (gag) AND 35Sb (gag-pol), 28S (env) mRNA"	
misc_RNA	<1..3176	
	/note="35S virion RNA"	
intron	<1..1047	
	/note="21S (src) intron A"	
CDS	<1..743	
	/note="env-Pr95 polyprotein precursor"	
	/number=2	
	/codon_start=3	
	/protein_id="AAA42562.1"	
	/db_xref="GI:459676"	
	/translation="IPSRPVGFCYGLKLTMLAPKHTDILKLVNSRTGIRRRKSTS	
	HDDTCSDEVOLWGPTARIPASILAPGVAAQAALRIERLACWVKOANTLTSLGDL	
	LDDVSTIBHVLONRAIDIFLLAHGCGEDVAGCCFNLSQSESTOKKFLMKSHV	
	NKLVDSDLIGSWELRGFLPGGIGENAVHLKGLLGLVILLVLCPLQLMLCGNRR	
	KMLNNSISYHYEYKKLQKACGQPESRIV"	
mat_peptide	<1..740	
	/product="glycoprotein-85"	
mat_peptide	126..740	
	/product="glycoprotein-37"	
CDS	1123..2703	
	/note="src-p60 phosphoprotein"	
	/codon_start=1	
	/protein_id="AAA42563.1"	
	/db_xref="GI:459677"	
	/translation="MGSXSKPKPSORBSLEPPDSHGGFPASOTPNKTAADPTH	
	RPSRSFGVATEPKLFGGNTSDTVSPQAGALAGGTVTFVAYDYESWITDLSF	
	KXGERLQVNNTEGNWLAHSITTCGTYIPSNYVAPSDISQABEWYFGKITRRESR	
	LLNPNENRGFTFLVSHADGLCHRLTNVCPSTQPKQGLADAMEIPRESLRLVKGQ	
	QSSSQIIVAYYSKHADGLCHRLTNVCPSTQPKQGLADAMEIPRESLRLVKGQ	
	YIVFVMSGLSLDLFLKGMGKYLLELPOLVMAAQIAGSMAYVERMNVHRDRAANI	
	LVGENLVCKVADFLGLARLIEDNEYTAQCGAKFFIKWTAPEALYGRFTIKSDYWSGI	
	LUETLTTKGRVFPFGMGENVLDVRVERGYRNPCCPEPSLHDLMLCQWRDPEERT	
LTR	2927..3256	
	/note="3' LTR"	
conflict	2938	
	/citation=[12]	
repeat_region	3156..3176	
	/note="3' terminal repeat"	
ORIGIN		
Query Match	98.6%; Score 515.6; DB 14; Length 3256;	
Best Local Similarity	99.2%; Pred. No. 5.9e-146;	
Matches	518; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60	
Db	2668 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 2727	
Qy	61 ACAAGGCAAGGCTTACCGCAATTCATGAGATCGCTTAGGGTTAGGGCTTTTCG 120	
Db	2728 ACAAGGCAAGGCTTACCGCAATTCATGAGATCGCTTAGGGTTAGGGCTTTTCG 2787	
Qy	121 CTGCTTCGCGATGTACGGGCGCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTTAGG 180	
Db	2798 CTGCTTCGCGATGTACGGGCGCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTTAGG 2847	
Qy	181 CGAAAAGCGGGCTTCGGTTGTGTACGGGTTAGGATCCCTCAGGATATAGTAGTTTCGC 240	
Db	2848 CGAAAAGCGGGCTTCGGTTGTGTACGGGTTAGGATCCCTCAGGATATAGTAGTTTCGC 2907	
Qy	241 TTTTGCATAGGAGGGGGGAATAGTACTTATGCAACTACTCTTGTAAGTCTTGCAACATGG 300	



```

KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS       Fazio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.
TITLE         Multi-chrionic vectors for gene transfer protocols
JOURNAL       Patent: WO 03031630-A 2 17-APR-2003;
              Keryos Spa (IT)
FEATURES      Location/Qualifiers
              source
                1..4457
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
ORIGIN
Query Match      97.3%; Score 508.8; DB 6; Length 4457;
Best Local Similarity 99.4%; Pred. NO. 7e-144;
Matches 521; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

QY	1	CTGCTCCCTCCTCTGTGTGTTTGGAGTTCGCTGAGTAGTGCAGGACGAAATTTAAGCTACA	60
Db	457	CTGCTCCCTCCTCTGTGTGTTTGGAGTTCGCTGAGTAGTGCAGGACGAAATTTAAGCTACA	516
QY	61	ACAAGCGAAGCGCTTGACCGACAATTCGATCAAGAATCTCTTAGGTTAGCGGTTTTGCG	120
Db	517	ACAAGCGAAGCGCTTGACCGACAATTCGATCAAGAATCTCTTAGGTTAGCGGTTTTGCG	576
QY	121	CTGCTTTGGGATGTACGGGCGCAGATATTCGCGGTATCTGAGGGGACCTAGGHTGTGTTAGG	180
Db	577	CTGCTTTGGGATGTACGGGCGCAGATATTCGCGGTATCTGAGGGGACCTAGGHTGTGTTAGG	636
QY	181	CGAAAAGCGGGCGTTCGGTTGTACGGGTTAGGAGTCCCTCCTCAGGATATAGTAGTTTCGC	240
Db	637	CGAAAAGCGGGCGTTCGGTTGTACGGGTTAGGAGTCCCTCCTCAGGATATAGTAGTTTCGC	696
QY	241	TTTTTCGATAGGGAGGGGGAATGTATGCTTTATGCGATCTCTCTTAGTCTCTTGCAACATGG	300
Db	697	TTTTTCGATAGGGAGGGGGAATGTATGCTTTATGCGATCTCTCTTAGTCTCTTGCAACATGG	756

697	TTTTGCAATGGGAGGGGGAATGTAGCTTATAGCAATACCTTTGTAGTCTTTGCACATCGG	756
301	TAAAGATGAGTTAGCAACAATCGCTTTACAAGGAGAGAAAAAGACCGTCGCATGCGGATTTGG	360
757	TAAAGATGAGTTAGCAACAATCGCTTTACAAGGAGAGAAAAAGACCGTCGCATGCGGATTTGG	816
361	TGGAAGTAAAGTGGTACCATCGTCGCTTATTAGGAGGCAACAGACGGGCTCGACATGA	420
817	TGGAAGTAAAGTGGTACCATCGTCGCTTATTAGGAGGCAACAGACGGGCTCGACATGA	876
421	TTGGAAGAACCACTAAATTCGCATTCACAGAGAT-ATTGTATTAAAGTGCGCTAGCTCGAT	479
877	TTGGAAGAACCACTGAATTCGCATTTGCAGAGATAATTGTATTAAAGTGCGCTAGCTCGAT	936
480	ACAATTAACCCATTTTGACCAATTCAACAATTGTTGTGACCTTC	523
937	ACAATTAACCCATTTTGACCAATTCAACAATTGTTGTGACCTTC	980

RESULT 11	
LOCUS	AX743956/c
LENGTH	7334 bp      DNA
DEFINITION	Sequence 4 from Patent WO0301630.
ACCESSION	AX743956
VERSION	AX743956.1 GI:30722653
KEYWORDS	. synthetic construct artificial sequences.
SOURCE	ORGANISM
REFERENCE	1
AUTHORS	Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Orsini,G.
TITLE	Multi-micronic vectors for gene transfer protocols
JOURNAL	Patent: WO 03031630-A 4 17-APR-2003; Keryos Spa (IT)
FEATURES	Location/Qualifiers

source 1. .7334  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 97.3%; Score 508.8; DB 6; Length 7334;  
Best Local Similarity 99.4%; Pred. No. 7e-144;  
Matches 521; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 60  
DB 2300 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 2241  
QY 61 ACAAGGCAAGGCTTCACCGCAATTTGCATGAAGATCTGTAGGGTTAGCGTTTTCGG 120  
DB 2240 ACAAGGCAAGGCTTCACCGCAATTTGCATGAAGATCTGTAGGGTTAGCGTTTTCGG 2181  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTGAGGGGACPVAGGGTGTCTTTCAG 180  
DB 2180 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTGAGGGGACPVAGGGTGTCTTTCAG 2121  
QY 181 CGAAAGCGGGCTTCGCTTGTAGCGGTAGAGTCCCTCAGGATATAGTCTTCG 240  
DB 2120 CGAAAGCGGGCTTCGCTTGTAGCGGTAGAGTCCCTCAGGATATAGTCTTCG 2061  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
DB 2060 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 2001  
QY 301 TAAAGATAGTATGCAACATGCCCTTACAAGGAGAGAAAGACCCGTGATGCCGATGG 360  
DB 2000 TAAAGATAGTATGCAACATGCCCTTACAAGGAGAGAAAGACCCGTGATGCCGATGG 1941  
QY 361 TGGAGTAAAGGTGTACCATCGTCTTATAGGAGGCAACAGAGCGGTCTGCATGGA 420  
DB 1940 TGGAGTAAAGGTGTACCATCGTCTTATAGGAGGCAACAGAGCGGTCTGCATGGA 1881  
QY 421 TTGACGAACCACTAAATTCGCATTTGCAGAGAT-ATTGTATTAAAGTCCCTAGCTCGAT 479  
DB 1880 TTGACGAACCACTAAATTCGCATTTGCAGAGATTAATTGTATTAAAGTCCCTAGCTCGAT 1821  
QY 480 ACAATAAACGCCATTTGACCAATTCACCAATTTGGTGGCACCTC 523  
DB 1820 ACAATAAACGCCATTTGACCAATTCACCAATTTGGTGGCACCTC 1777

RESULT 12  
SYNRSV3MV  
LOCUS  
DEFINITION Cloning vector RSV3.  
ACCESSION M83240  
VERSION M83240.1 GI:209303  
KEYWORDS cDNA expression vector.  
SOURCE unidentified cloning vector  
ORGANISM artificial sequences; vectors.  
REFERENCE  
1 (sites)  
Messing,J.  
TITLE New M13 vectors for cloning  
JOURNAL Meth. Enzymol. 101, 20-78 (1983)  
MEDLINE 83296918  
PUBMED 6310323  
REFERENCE  
2 (sites)  
Gorman,C., Padmanabhan,R. and Howard,B.H.  
TITLE High efficiency DNA-mediated transformation of primate cells  
JOURNAL Science 221 (4610), 551-553 (1983)  
MEDLINE 8349156  
PUBMED 6306768  
REFERENCE  
3 (bases 1 to 3557)  
Jacobson,S., Sekaly,R.P., Jacobson,C.L., McFarland,H.P. and Long,E.O.  
TITLE HLA class II-restricted presentation of cytoplasmic measles virus

antigens to cytotoxic T cells  
J. Virol. 63 (4), 1756-1762 (1989)  
MEDLINE 89178963  
PUBMED 2784508  
COMMENT Original source text: Cloning vector DNA.  
FEATURES  
source  
1. .3557  
Location/Qualifiers  
/organism="unidentified cloning vector"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:45196"  
1. .29  
/function="polylinker"  
/evidence=experimental  
912. .3029  
misc\_feature  
/function="ampicillin-resistance, replication origin"  
/evidence=experimental  
3030. .3557  
enhancer  
/standard\_name="5'LTR of Rous Sarcoma Virus"  
/citation=[2]  
/evidence=experimental

ORIGIN

Query Match 96.7%; Score 505.6; DB 12; Length 3557;  
Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 60  
DB 3030 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTTAGCTACA 3089  
QY 61 ACAAGGCAAGGCTTCACCGCAATTTGCATGAAGATCTGTAGGGTTAGCGTTTTCGG 120  
DB 3090 ACAAGGCAAGGCTTCACCGCAATTTGCATGAAGATCTGTAGGGTTAGCGTTTTCGG 3149  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTCAGGGGACPVAGGGTGTCTTTCAG 180  
DB 3150 CTGCTTCGGATGTACGGGCCAGATATTCGCTATCTCAGGGGACPVAGGGTGTCTTTCAG 3209  
QY 181 CGAAAGCGGGCTTCGCTTGTACCGGTTAGGAGTCCCTCAGGATATAGTCTTCG 240  
DB 3210 CGAAAGCGGGCTTCGCTTGTACCGGTTAGGAGTCCCTCAGGATATAGTCTTCG 3269  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
DB 3270 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 3329  
QY 301 TAAAGATAGTATGCAACATGCCCTTACAAGGAGAGAAAGACCCGTGATGCCGATGG 360  
DB 3330 TAAAGATAGTATGCAACATGCCCTTACAAGGAGAGAAAGACCCGTGATGCCGATGG 3389  
QY 361 TGGAGTAAAGGTGTACCATCGTCTTATAGGAGGCAACAGAGCGGTCTGCATGGA 420  
DB 3390 TGGAGTAAAGGTGTACCATCGTCTTATAGGAGGCAACAGAGCGGTCTGCATGGA 3449  
QY 421 TTGACGAACCACTAAATTCGCATTTGCAGAGAT-ATTGTATTAAAGTCCCTAGCTCGAT 479  
DB 3450 TTGACGAACCACTAAATTCGCATTTGCAGAGATTAATTGTATTAAAGTCCCTAGCTCGAT 3509  
QY 480 ACAATAAACGCCATTTGACCAATTCACCAATTTGGTGGCACCTC 523  
DB 3510 ACAATAAACGCCATTTGACCAATTCACCAATTTGGTGGCACCTC 3553

RESULT 13  
AR071324/c  
LOCUS  
DEFINITION Sequence 2 from patent US 5910488.  
ACCESSION AR071324  
VERSION AR071324.1 GI:7222212  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 4059)  
AUTHORS Nabel, G.J., Nabel, E.G., Lew, D. and Marquet, M.  
TITLE Plasmids suitable for gene therapy  
JOURNAL Patent: US 5910488-A 2 08-JUN-1999;  
FEATURES Location/Qualifiers  
source 1. 4059  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 96.7%; Score 505.6; DB 6; Length 4059;  
Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
Db 3415 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 3356  
Qy 61 ACAAGGCAAGGCTTGACCGACAATTTGCAATGAAGAATCTGCTTAGGGTTAGGGCTTTTGG 120  
Db 3355 ACAAGGCAAGGCTTGACCGACAATTTGCAATGAAGAATCTGCTTAGGGTTAGGGCTTTTGG 3296  
Qy 121 CTGCTCCGATGTACGGCCAGATATTCGGTATCTGAGGGAGCTAGGCTGTGTTAGG 180  
Db 3295 CTGCTCCGATGTACGGCCAGATATTCGGTATCTGAGGGAGCTAGGCTGTGTTAGG 3236  
Qy 181 CGAAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
Db 3235 CGAAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 3176  
Qy 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGG 300  
Db 3175 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGG 3116  
Qy 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360  
Db 3115 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 3056  
Qy 361 TGGAGTAAGTGTGATCGATCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420  
Db 3055 TGGAGTAAGTGTGATCGATCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 2956  
Qy 421 TTGGACGAACCACTAAATTCGGATTTGAGAGAT-ATTGTATTTAAGTGTGCTAGCTCGAT 479  
Db 2955 TTGGACGAACCACTAAATTCGGATTTGAGAGAT-ATTGTATTTAAGTGTGCTAGCTCGAT 2936  
Qy 480 ACAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCACTC 523  
Db 2935 ACAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCACTC 2892

RESULT 14  
A38214  
LOCUS A38214 4341 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 58 from Patent WO9408008.  
ACCESSION A38214  
VERSION A38214.1 GI:2294819  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 4341)  
AUTHORS Hawkins, R.E., Russell, S.J., Stevenson, F.K. and Winter, G.P.  
TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION  
JOURNAL Patent: WO 9408008-A 58 14-APR-1994;  
MEDICAL RES COUNCIL (GB)  
COMMENT Other publication CA 2145064 940414  
Other publication AU 4832493 940426  
Other publication JP 85016997 960227.  
FEATURES Location/Qualifiers  
source 1. 4341  
/organism="unidentified"  
/mol\_type="unassigned DNA"

/db\_xref="taxon:32644"

ORIGIN  
Query Match 96.7%; Score 505.6; DB 6; Length 4341;  
Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 140  
Qy 61 ACAAGCAAGGCTTGACCGACAATTTGCAATGAAGAATCTGCTTAGGGTTAGGGCTTTTGG 120  
Db 141 ACAAGCAAGGCTTGACCGACAATTTGCAATGAAGAATCTGCTTAGGGTTAGGGCTTTTGG 200  
Qy 121 CTGCTCCGATGTACGGCCAGATATTCGGTATCTGAGGGAGCTAGGCTGTGTTAGG 180  
Db 201 CTGCTCCGATGTACGGCCAGATATTCGGTATCTGAGGGAGCTAGGCTGTGTTAGG 260  
Qy 181 CGAAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
Db 261 CGAAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 320  
Qy 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGG 300  
Db 321 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGG 380  
Qy 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360  
Db 381 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 440  
Qy 361 TGGAGTAAGTGTGATCGATCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420  
Db 441 TGGAGTAAGTGTGATCGATCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 500  
Qy 421 TTGGACGAACCACTAAATTCGGATTTGAGAGAT-ATTGTATTTAAGTGTGCTAGCTCGAT 479  
Db 501 TTGGACGAACCACTAAATTCGGATTTGAGAGAT-ATTGTATTTAAGTGTGCTAGCTCGAT 560  
Qy 480 ACAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCACTC 523  
Db 561 ACAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCACTC 604

RESULT 15  
AX286570  
LOCUS AX286570 4341 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 1 from Patent WO0179510.  
ACCESSION AX286570  
VERSION AX286570.1 GI:17048664  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Rice, J.H. and Stevenson, F.M.  
TITLE Materials and methods relating to immune responses to fusion proteins  
JOURNAL Patent: WO 0179510-A 1 25-OCT-2001;  
Cancer Research Ventures Limited (GB)  
FEATURES Location/Qualifiers  
source 1. 4341  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Vector pVAC1"

ORIGIN  
Query Match 96.7%; Score 505.6; DB 6; Length 4341;  
Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60

```
Db      81  CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140
Qy      61  ACAAGCAGAGGCTTACCGACAAATTCATGAAGATCTCTTAGGTTAGCGGTTTTGG 120
Db      141  ACAGGCAAGGCTTGACCGCAATTCATGAAGATCTCTTAGGTTAGCGGTTTTGG 200
Qy      121  CTGCTTCGCGATGTACGCGCCAGATATTCGCTATCTTGAGGGGACTAGGCTGTGTTAGG 180
Db      201  CTGCTTCGCGATGTACGCGCCAGATATACGCGTATCTTGAGGGGACTAGGCTGTGTTAGG 260
Qy      181  CGAAAGCGGGCTTCGGTTGTACGCGGTTAGAGTCCCTCAGGATATAGTAGTTCCG 240
Db      261  CGAAAGCGGGCTTCGGTTGTACGCGGTTAGAGTCCCTCAGGATATAGTAGTTCCG 320
Qy      241  TTTTGCATAGGAGGAGGAAATCTAGCTTATGCAATCTCTTGAGTCTTGCAACATGG 300
Db      321  TTTTGCATAGGAGGAGGAAATCTAGCTTATGCAATCTCTTGAGTCTTGCAACATGG 380
Qy      301  TAACGATGTAGTACCATGCTTACAGGAGAGAAAGCACCGTGCAATGCCGATTGG 360
Db      381  TAACGATGTAGTACCATGCTTACAGGAGAGAAAGCACCGTGCAATGCCGATTGG 440
Qy      361  TCGAGCTAGGTTGTCGACGCGCTTATAGGAGGCAACAGCGGCTGACATGGA 420
Db      441  TCGAGCTAGGTTGTCGACGCGCTTATAGGAGGCAACAGCGGCTGACATGGA 500
Qy      421  TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479
Db      501  TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 560
Qy      480  ACAATAAGCGCATTTGACCAATTCACCAATTTGGTGTGCACCTC 523
Db      561  ACAATAAGCGCATTTGACCAATTCACCAATTTGGTGTGCACCTC 604

RESULT 16
SYNRSV5GPT  SYNRSV5GPT  4839 bp  DNA  circular SYN 16-MAR-2000
LOCUS      Cloning vector RSV.5(gpt).
DEFINITION M83236
ACCESSION  M83236
VERSION    M83236.1 GI:209304
KEYWORDS   cDNA expression vector.
SOURCE     Cloning vector pUC19
ORGANISM   artificial sequences; vectors.
REFERENCE  1 (bases 1 to 4839)
AUTHORS    Long,E.O., Rosen-Bronson,S., Kaip,D.R., Malnati,M., Sekaly,R.P. and
            Jaramenada,D.
TITLE      Efficient cDNA expression vectors for stable and transient
            expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL    Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE    92011006
PUBMED     1655683
FEATURES   Location/Qualifiers
            source
            1..4839
            /organism="Cloning vector pUC19"
            /mol_type="genomic DNA"
            /db_xref="taxon:31851"
            /focus
            1..29
            /organism="Cloning vector pUC12"
            /mol_type="genomic DNA"
            /db_xref="taxon:83674"
            /note="HindIII to BamHI fragment of pUC12"
            30..872
            /organism="Simian virus 40"
            /mol_type="genomic DNA"
            /db_xref="taxon:10633"
            /note="Bi-directional SV40 termination and
            poly-adenylation sequences."
            873..1929
            /organism="Escherichia coli"
```

```
source
/mol_type="genomic DNA"
/db_xref="taxon:562"
1930..2273
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
2274..4311
/note="SV40 early promoter and origin of replication."
source
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/note="Ampicillin resistance gene and origin of replication
from the vector pBR322."
4312..4839
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11886"
/note="5' long terminal repeat."
1..29
/function="polylinker"
/evidence=experimental
misc_feature
/product="guanine-hypoxanthine phosphoribosyltransferase"
/standard_name="gpt"
/note="gpt gene from E.coli, putative mature peptide -
contains internal stop codons; putative"
2274..4311
/function="ampicillin resistance and origin of
replication"
/evidence=experimental

ORIGIN

Query Match 96.7%; Score 505.6; DB 12; Length 4839;
Best Local Similarity 99.0%; Pred. No. 6.6e-143;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy      1  CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60
Db      4312  CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 4371
Qy      61  ACAAGCAGAGGCTTACCGACAAATTCATGAAGATCTCTTAGGTTAGCGGTTTTGG 120
Db      4372  ACAAGCAGAGGCTTACCGACAAATTCATGAAGATCTCTTAGGTTAGCGGTTTTGG 4431
Qy      121  CTGCTTCGCGATGTACGCGCCAGATATTCGCTATCTTGAGGGGACTAGGCTGTGTTAGG 180
Db      4432  CTGCTTCGCGATGTACGCGCCAGATATACGCTATCTTGAGGGGACTAGGCTGTGTTAGG 4491
Qy      181  CGAAAGCGGGCTTCGGTTGTACGCGGTTAGGATCCCTCAGGATATAGTAGTTCCG 240
Db      4492  CGAAAGCGGGCTTCGGTTGTACGCGGTTAGGATCCCTCAGGATATAGTAGTTCCG 4551
Qy      241  TTTTGCATAGGAGGAGGAAATGTAGCTTATGCAATCTCTTGAGTCTTGCAACATGG 300
Db      4552  TTTTGCATAGGAGGAGGAAATGTAGCTTATGCAATCTCTTGAGTCTTGCAACATGG 4611
Qy      301  TAACGATGTAGTACCAATTCGCTTACAGGAGAGAAAGCACCGTGCNTGCCGATTGG 360
Db      4612  TAACGATGTAGTACCAATTCGCTTACAGGAGAGAAAGCACCGTGCNTGCCGATTGG 4671
Qy      361  TGGAGTAAAGTGTGATGATCTGCTTATAGGAGGCAACAGAGGCTGTGACATGGA 420
Db      4672  TGGAGTAAAGTGTGATGATCTGCTTATAGGAGGCAACAGAGGCTGTGACATGGA 4731
Qy      421  TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479
Db      4732  TTGAGCAACCACTGAATTCGCAATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 4791
Qy      480  ACAATAAGCGCATTTGACCAATTCACCAATTTGGTGTGCACCTC 523
Db      4792  ACAATAAGCGCATTTGACCAATTCACCAATTTGGTGTGCACCTC 4835
```

```

RESULT 17
SYNRSV5NEO      5108 bp      DNA      linear      SYN 06-APR-2001
LOCUS           cDNA expression vector RSV.5(neo) .
DEFINITION      M83237
ACCESSION       M83237.1 GI:209305
VERSION         cDNA expression vector.
KEYWORDS        Expression vector RSV.5(neo)
SOURCE          Expression vector RSV.5(neo)
ORGANISM        artificial sequences; vectors.
REFERENCE       1 (bases 1 to 5108)
AUTHORS         Long,E.O., Rosen-Bronson,S., Karp,D.R., Malmati,M., Sekaly,R.P. and
                Jaraquemada,D.
TITLE           Efficient cDNA expression vectors for stable and transient
                expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL         Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE         92011006
PUBMED          1655683
FEATURES        Location/Qualifiers
                 1..5108
                 /organism="Expression vector RSV.5(neo)"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:118308"
                 /focus
                 1..29
                 /organism="unidentified cloning vector"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:45196"
                 /note="HindIII to BamHI fragment of pUC12."
                 30..872
                 /organism="Simian virus 40"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:10633"
                 /note="Bi-directional SV40 termination and
                 poly-adenylation sequence."
                 873..879
                 /organism="unidentified cloning vector"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:45196"
                 /note="Remnant of gpt gene from the cDNA expression vector
                 RSV.5(gpt)."
                 880..2197
                 /organism="Cloning vector pSV2neo"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:31846"
                 /note="TN5 neomycin-resistance gene from cloning vector
                 pSV2neo."
                 2198..2542
                 /organism="Simian virus 40"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:10633"
                 /note="SV40 early promoter and origin of replication."
                 2543..4580
                 /organism="Cloning vector pBR322"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:47470"
                 /note="Ampicillin resistance gene and origin of
                 replication from pBR322."
                 4581..5108
                 /organism="Rous sarcoma virus"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:11886"
                 /note="5' long terminal repeat of Rous Sarcoma virus."
                 1..29
                 /function="polylinker"
                 /evidence=experimental
                 complement(880..2197)
                 /note="neomycin resistance gene from pSV2neo, putative
                 mature peptide - contains internal stop codons; putative"
                 2543..4580
                 /product="ampicillin resistance"
                 /function="ampicillin resistance and origin of
                 replication"

```

```

/evidence=experimental
4581..5108
/standard_name="5'LTR of Rous Sarcoma Virus"
/function="promoter"
/evidence=experimental

ORIGIN
Query Match      96.7%; Score 505.6; DB 12; Length 5108;
Best Local Similarity 99.0%; Pred. No. 6.6e-143;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTGCGCTGAGTAGTGCAGGAGCAAAATTTAAAGTACA 60
Db 4581 CTGCTCCCTGCTGTGTGTGGAGGTGCGCTGAGTAGTGCAGGAGCAAAATTTAAAGTACA 4640
Qy 61 ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGCTTAGGGTTAGGGTTTGG 120
Db 4641 ACAGGCAAGGCTTACCGCAATTCATGAAGATCTGCTTAGGGTTAGGGTTTGG 4700
Qy 121 CTGCTTCGGGATGTACGGGCGAGATATTCGGGTATCTGAGGGACTAGGGTGTCTTAGG 180
Db 4701 CTGCTTCGGGATGTACGGGCGAGATATTCGGGTATCTGAGGGACTAGGGTGTCTTAGG 4760
Qy 181 CGAAAAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTTGCG 240
Db 4761 CGAAAAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTTGCG 4820
Qy 241 TTTTGCATAGGGGAGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300
Db 4821 TTTTGCATAGGGGAGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 4880
Qy 301 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGG 360
Db 4881 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGG 4940
Qy 361 TGGAGTAAAGTGGTACATCGTGCCTTATTTAGAGAGCAACAGAGGGTCTGACATGGA 420
Db 4941 TGGAGTAAAGTGGTACATCGTGCCTTATTTAGAGAGCAACAGAGGGTCTGACATGGA 5000
Qy 421 TTGGAGCAACACATTAATTCGGCATTTGCAGATGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 479
Db 5001 TTGGAGCAACACATTAATTCGGCATTTGCAGATGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 5060
Qy 480 ACAATAAAGCCATTTGACCATTCACCATTTGGTGTGACCTC 523
Db 5061 ACAATAAAGCCATTTGACCATTCACCATTTGGTGTGACCTC 5104

RESULT 18
SYNRCRC
LOCUS           5564 bp      DNA      linear      SYN 27-SEP-1994
DEFINITION      Cloning vector murine T-cell receptor C-beta 1 DNA, 3' end of cds.
ACCESSION       L36555
VERSION         L36555.1 GI:550523
KEYWORDS        T-cell receptor C-beta 1; T-cell receptor V-beta; cloning vector.
SOURCE          unidentified cloning vector
ORGANISM        artificial sequences; vectors.
REFERENCE       1 (bases 1 to 5564)
AUTHORS         Palmer,M.S., Bentley,A., Gould,K. and Townsend,A.R.
TITLE           The T cell receptor from an influenza-A specific murine CTL clone
JOURNAL         Nucleic Acids Res. 17 (6), 2353 (1989)
MEDLINE         89202046
PUBMED          2784852
REFERENCE       2 (bases 1 to 5564)
AUTHORS         Long,E.O., Rosen-Bronson,S., Karp,D.R., Malmati,M., Sekaly,R.P. and
                Jaraquemada,D.
TITLE           Efficient cDNA expression vectors for stable and transient
                expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL         Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE         92011006
PUBMED          1655683
REFERENCE       3 (bases 1 to 5564)

```

AUTHORS Denis,F., Soudeyrs,H., Ringette,N. and Sekaly,R.-P.  
 TITLE A simple method for the cloning and functional expression of human T cell receptor Vbeta segments in murine hybridomas  
 JOURNAL Unpublished (1994)  
 COMMENT Original source text: Cloning vector DNA.  
 FEATURES Location/Qualifiers  
 source 1..5564  
 /organism="unidentified cloning vector"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:45196"

CDS  
 <13..480  
 /note="murine"  
 /citation=[3]  
 /codon\_start=1  
 /evidence=experimental  
 /transl\_table=11  
 /product="T-cell receptor C beta 1"  
 /protein\_id="AA07448.1"  
 /db\_xref="GI:550524"  
 /translation="VDIAKQKATLVCLAGFFPDHVELSWYNGKEVHSGVSTDPQA  
 YKSNVYCLSSRLRVSATFWHPRNHFRCQVQPHGLSEEDKWPESKPVQVQISAE  
 AWGRADCGITTSASVHQVLSATILYELLKATLVAVLVSLVIMAMVKKNS"

ORIGIN

Query Match 96.7%; Score 505.6; DB 12; Length 5564;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60  
 DB 5037 CTGCTCCCTGCTTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 5096  
 DB 5097 ACAGGCAAGGCTGACCGACAAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGG 120  
 QY 61 ACAGGCAAGGCTGACCGACAAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGG 120  
 DB 5097 ACAGGCAAGGCTGACCGACAAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGG 5156  
 QY 121 CTGCTTCGGAGTACCGGCGCAGATTCGCGTATCTGAGGGGACTAGGGTGTATTAG 180  
 DB 5157 CTGCTTCGGAGTACCGGCGCAGATTCGCGTATCTGAGGGGACTAGGGTGTATTAG 5216  
 QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
 DB 5217 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 5276  
 QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 300  
 DB 5277 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 5336  
 QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCGATTGG 360  
 DB 5337 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCGATTGG 5396  
 QY 361 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGCTCGACATGGA 420  
 DB 5397 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGCTCGACATGGA 5456  
 QY 421 TTGAGCAACACCACTAAATTCGCAATTCGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479  
 DB 5457 TTGAGCAACACCACTAAATTCGCAATTCGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 5516  
 QY 480 ACATTAACGCCATTTCACCATTCACCATTCACCATTCACCATTCACCATTCACCATTC 523  
 DB 5517 ACATTAACGCCATTTCACCATTCACCATTCACCATTCACCATTCACCATTCACCATTC 5560

RESULT 19  
 LOCUS I56772  
 DEFINITION Sequence 3 from patent US 5650306.  
 ACCESSION I56772  
 VERSION I56772.1 GI:2477185  
 KEYWORDS  
 SOURCE Unknown.

ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5653)  
 AUTHORS Nabel,G.J., Yang,Z.-Y., Liu,J. and Woffendin,C.  
 TITLE Recombinant nucleic acids for inhibiting HIV gene expression  
 JOURNAL Patent: US 5650306-A 3 22-JUL-1997;  
 FEATURES Location/Qualifiers  
 source 1..5653  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 ORIGIN  
 Query Match 96.7%; Score 505.6; DB 6; Length 5653;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60  
 DB 81 CTGCTCCCTGCTTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 140  
 QY 61 ACAGGCAAGGCTTGCACGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGG 120  
 DB 141 ACAGGCAAGGCTTGCACGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGG 200  
 QY 121 CTGCTTCGGAGTACCGGCGCAGATTCGCGTATCTGAGGGGACTAGGGTGTATTAG 180  
 DB 201 CTGCTTCGGAGTACCGGCGCAGATTCGCGTATCTGAGGGGACTAGGGTGTATTAG 260  
 QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
 DB 261 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 320  
 QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 300  
 DB 321 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 380  
 QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCGATTGG 360  
 DB 381 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCGATTGG 440  
 QY 361 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGCTCGACATGGA 420  
 DB 441 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGCTCGACATGGA 500  
 QY 421 TTGAGCAACACCACTAAATTCGCAATTCGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479  
 DB 501 TTGAGCAACACCACTAAATTCGCAATTCGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 560  
 QY 480 ACATTAACGCCATTTCACCATTCACCATTCACCATTCACCATTCACCATTCACCATTC 523  
 DB 561 ACATTAACGCCATTTCACCATTCACCATTCACCATTCACCATTCACCATTCACCATTC 604  
 RESULT 20  
 LOCUS I95540  
 DEFINITION Sequence 1 from patent US 5733543.  
 ACCESSION I95540  
 VERSION I95540.1 GI:3940010  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5653)  
 AUTHORS Nabel,G.J., Woffendin,C., Yang,N.-S. and Sheehy,M.J.  
 TITLE Introduction of HIV-protective genes into cells by particle-mediated gene transfer  
 JOURNAL Patent: US 5733543-A 1 31-MAR-1998;  
 FEATURES Location/Qualifiers  
 source 1..5653  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 ORIGIN



Query Match 96.7%; Score 505.6; DB 6; Length 5653;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGAACGCAATTCATGAAGATCTGCTTAGGTTAGGCGTTTGGC 120  
 Db 141 ACAAGGCAAGGCTTGAACGCAATTCATGAAGATCTGCTTAGGTTAGGCGTTTGGC 200

Qy 121 CTGCTTCGGGATGTAACGGGCAATTCATGAAGATCTGCTTAGGTTAGGCGTTTGGC 180  
 Db 201 CTGCTTCGGGATGTAACGGGCAATTCATGAAGATCTGCTTAGGTTAGGCGTTTGGC 260

Qy 181 CGAAAAGCGGGCTTCGGTTGTACGGGTCAGTCCCTCAGGATATAGTAGTTTCGC 240  
 Db 261 CGAAAAGCGGGCTTCGGTTGTACGGGTCAGTCCCTCAGGATATAGTAGTTTCGC 320

Qy 241 TTTTGCATAGGAGGGGAAATGAGTCTTATGCACTACTCTGTAGTCTTGCACATGG 300  
 Db 321 TTTTGCATAGGAGGGGAAATGAGTCTTATGCACTACTCTGTAGTCTTGCACATGG 380

Qy 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 360  
 Db 381 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 440

Qy 361 TGGAGTAGAGGTGTAAGTCTGCTTATAGGAGGCAACAGCGGTCTGACATGA 420  
 Db 441 TGGAGTAGAGGTGTAAGTCTGCTTATAGGAGGCAACAGCGGTCTGACATGA 500

Qy 421 TTGAGCAACACCTAATTCGGCATTCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 479  
 Db 501 TTGAGCAACACCTAATTCGGCATTCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 560

RESULT 21  
 SYNPRSVNeo/c  
 LOCUS SYNPRSVNeo 5736 bp DNA circular SYN 27-APR-1993  
 DEFINITION PRSVNeo cloning vector for high efficiency gene transfer into mammalian cells.  
 ACCESSION M77786  
 VERSION M77786.1 GI:209147  
 SOURCE synthetic construct  
 KEYWORDS synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 5736)  
 AUTHORS Gilbert.W.  
 TITLE Obtained from VecBase 3.0  
 JOURNAL Unpublished (1991)  
 COMMENT Original source text: Synthetic construct DNA.  
 These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program. PRSVNeo - Cloning Vector for High Efficiency Gene Transfer into Mammalian Cells  
 ENTRY PRSVNeo #TYPE DNA CIRCULAR TITLE PRSVNeo - Cloning Vector for High Efficiency Gene Transfer into Mammalian Cells  
 DATE 06-JUN-1986  
 #sequence 16-DEC-1986  
 ACCESSION V00064  
 SOURCE artificial  
 COLLECTION ATCC 37198  
 REFERENCE  
 #number 1  
 #authors Gorman C.

#book 'DNA cloning Volume II, a practical approach', pp. 143-190,  
 edited by D. M. Glover, IRL Press, (1986),  
 eds. D. Rickwood and B. D. Hames

COMMENT  
 Entered by William Gilbert, Whitaker College, MIT, 02-APR-1986  
 Revised 16-DEC-1986 by F. Pfeiffer:  
 1012/3 'AT' to 'TA' to match revised sequence of PBR322 KEYWORDS  
 CROSSREFERENCE  
 #parent  
 VecBase (3): PBR322, GenBank (50): SV40G,  
 GenBank (50): ALRPROLTH,  
 GenBank (50): Trn5Neo, GenBank (50): Trn5IR1

PARENT  
 Features of PRSVNeo (5736 bp)  
 residue source  
 6- 529 550- 27 (c) Rous Sarcoma Virus (GenBank (50):  
 ALRPROLTH)  
 6- 529 3189-2667 (c) GenBank (50): ALRPROLTH (6 mutations)  
 529-2644 1781-2774 SV40  
 2641-3634 1781-2774 SV40  
 3631-4244 4100-4713 SV40  
 4248-5533 1286- 1 (c) Trn5 (GenBank (50): TRN5NEO)  
 5251-5736 1720-1235 (c) Trn5 (GenBank (50): TRN5IR1)  
 Conflict (cfl) and Mutations (mut): none

FEATURE  
 1579-2367 789-1 (c) Ap-R; b-lactamase  
 4589-5383 791-1 (c) Neo-R

POLYLINKER  
 SELECTION #resistance Ap  
 SUMMARY PRSVNeo #length 5736 #checksum 3569.  
 Location/Qualifiers  
 source  
 1. .5736  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

ORIGIN  
 Query Match 96.7%; Score 505.6; DB 12; Length 5736;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGTGGAGTGGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
 Db 528 CTGCTCCCTGCTGTGTGTGGAGTGGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 469

Qy 61 ACAAGGCAAGGCTTGAACGCAATTCATGAAGATCTGCTTAGGTTAGGCGTTTGGC 120  
 Db 468 ACAAGGCAAGGCTTGAACGCAATTCATGAAGATCTGCTTAGGTTAGGCGTTTGGC 409

Qy 121 CTGCTTCGGGATGTAACGGGCAATTCATGAAGATCTGCTTAGGTTAGGCGTTTGGC 180  
 Db 408 CTGCTTCGGGATGTAACGGGCAATTCATGAAGATCTGCTTAGGTTAGGCGTTTGGC 349

Qy 181 CGAAAAGCGGGCTTCGGTTGTACGGGTCAGTCCCTCAGGATATAGTAGTTTCGC 240  
 Db 348 CGAAAAGCGGGCTTCGGTTGTACGGGTCAGTCCCTCAGGATATAGTAGTTTCGC 289

Qy 241 TTTTGCATAGGAGGGGAAATGAGTCTTATGCACTACTCTGTAGTCTTGCACATGG 300  
 Db 288 TTTTGCATAGGAGGGGAAATGAGTCTTATGCACTACTCTGTAGTCTTGCACATGG 229

Qy 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 360  
 Db 228 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 169

Qy 361 TGGAGTAGAGGTGTAAGTCTGCTTATAGGAGGCAACAGCGGTCTGACATGA 420  
 Db 168 TGGAGTAGAGGTGTAAGTCTGCTTATAGGAGGCAACAGCGGTCTGACATGA 109

Qy 421 TTGAGCAACACCTAATTCGGCATTCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 479  
 Db 108 TTGAGCAACACCTAATTCGGCATTCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 49

QY 480 ACATTAAGCGCATTCACCATTCACCATTCGGTGGACCTC 523  
 Db 48 ACATTAAGCGCATTCACCATTCACCATTCGGTGGACCTC 5

RESULT 22  
 XXU19931 6864 bp DNA linear SYN 30-MAR-1995  
 LOCUS Cloning vector pGlaRSV, complete sequence.  
 DEFINITION  
 ACCESSION U19931  
 VERSION U19931.1 GI:644834  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Cloning vector pGlaRSV  
 Cloning vector pGlaRSV  
 artificial sequences, vectors.  
 REFERENCE  
 1 (bases 1 to 6864)  
 AUTHORS Gottgens,B.B.  
 TITLE A versatile lacZ reporter vector  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 641 to 4011)  
 AUTHORS Ravid,K., Beeler,D.L., Rabin,M.S., Ruley,H.E. and Rosenberg,R.D.  
 TITLE Selective targeting of gene products with the megakaryocyte platelet factor 4 promoter  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1521-1525 (1991)  
 MEDLINE 91142205  
 PUBMED 1899930  
 REFERENCE 3 (bases 1 to 6864)  
 AUTHORS Gottgens,B.B.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JAN-1995) Berthold B. Gottgens, Hematology, Cambridge University, MRC Centre, Hills Road, Cambridge, UK, CB2 2QH  
 FEATURES  
 source  
 1. .37  
 /notes="obtained from pGlaRSV"  
 /organism="Cloning vector pGlaRSV"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:39038"  
 misc\_feature  
 1. .37  
 /notes="obtained from pGlaRSV, Genbank Accession Number U19930"  
 misc\_feature  
 38. .631  
 /notes="RSV LTR from pRC/RSV cloned as a BglII/HindIII fragment"  
 misc\_feature  
 632. .6864  
 /notes="obtained from pGlaRSV, Genbank Accession Number U19930"  
 misc\_feature  
 641. .4011  
 /notes="obtained from pSDKlacZpA containing the E. coli lacZ gene followed by an SV40 polyA site"  
 /citation=[2]  
 662. .3727  
 /genes="lacZ"  
 662. .3727  
 /genes="lacZ"  
 /codon\_start=1  
 /transl\_table=1  
 /product="b-galactosidase"  
 /protein\_id="AA64569.1"  
 /db\_xref="GI:644835"  
 /translation="WARDPPVLQQRDQWENPGVITLNRLAAHPFPASWRNSERATDR  
 PSQRLSNGERRFAWEPAPESWLECDLEADTVVPSNMQMGYDAPLYTNT  
 YPIVNPFPPEAPTCYSLITNVDSWLGQGTLLFDGVNSAPHLWNCGRWVG  
 QDRLEPSEFSAFRAGENLAWVLRWSGSLYEDQDMRMSGIFDFVSLLRKPT  
 QISDFHVAFRNDFRSLVLAEEVQWCELDRLVTVSLWQGTQVASTGAPFGEI  
 IDRGYADRVTLNVRNHEHPLHGVMDQTVQDILLKONFNFAVGRSHVFN  
 IENGLLNGKPLIRGVNHEHPLHGVMDQTVQDILLKONFNFAVGRSHVFN  
 HPLWYLLCDRGLYVDEANIEFGWPMRLTDDPRLPAMSEVETMQRDRNPS  
 VTIWLSGNSGEGHANALRWIKSVDSRPVQYEGGADTTADICPMYARVDEQ  
 PFWAPKWSIKKWLSPGERTPLICEYAHAMGNSLGGFAKYWQAFRPLRQGGFVW  
 DVQDQLIKYDNGNPSAYGDFGTFNDPQFCMGLVFADRTPEALTEAKHQOF  
 FQRLSGQTIETVEYLFRHSNDLHMVADLGKPLASGEVLPDPAQKQILPE  
 LPOESAGQWLTVVQPNATWSAGHISAWQWELAEISVLPAAHAIPLHTT  
 SEMDFCLGKRWQNRQSGFLSQMWIGDKKQLLTPLRQFTRAPLNDIGVSEATR

misc\_feature  
 /notes="vector backbone from pGI-2basic, Genbank Accession  
 Number X65323"  
 complement (5081..5941)  
 /gene="bla"  
 complement (5081..5941)  
 /gene="bla"  
 /codon\_start=1  
 /transl\_table=1  
 /product="beta-lactamase"  
 /protein\_id="AA64570.1"  
 /db\_xref="GI:644836"  
 /translation="MSIQHFRVALIPFAAEFLPFAHPETLVKVKDAEDQLGARVGY  
 IEIDLNSKILESFRPRFPMMSTFKVLGAVLSRIDAGQEQLGRRIHYSQNDLAVE  
 YSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLLTIGPKELTAFILMHWDRVTRL  
 DRWEPELNEATPDERDITPMVAMATTIRKLTLGELLTLASRQQLIDMWADKVGFL  
 LRSALPAGWFIADKSGAGERSGRIIAALGDPGKPSRIIVITYTGSQATMDERNQIA  
 EIGASLIKHW"

ORIGIN  
 Query Match 96.7%; Score 505.6; DB 12; Length 6864;  
 Best Local Similarity 99.0%; Pred. No. 6.6e-143;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTCTGTGTGTCGAGTGTAGTGTGCGGAGCAAAATTTAAGCTACA 60  
 Db 106 CTGCTCCCTCTGTGTGTCGAGTGTAGTGTGCGGAGCAAAATTTAAGCTACA 165  
 QY 61 ACAAGGCAAGGCTTGACGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGG 120  
 Db 166 ACAAGGCAAGGCTTGACGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGG 225  
 QY 121 CTGCTTGGCATGTACGGCCAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 180  
 Db 226 CTGCTTGGCATGTACGGCCAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 285  
 QY 181 CGAAAAGCGGGCTTCGGTTGTAGCGTTTAGGATGCCCTCAGGATATAGTAGTTTCG 240  
 Db 286 CGAAAAGCGGGCTTCGGTTGTAGCGTTTAGGATGCCCTCAGGATATAGTAGTTTCG 345  
 QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Db 346 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 405  
 QY 301 TAAAGCATGTAGCAACATGCTTACAGGAGAGAAAACGCGTGCATGCCATTGG 360  
 Db 406 TAAAGCATGTAGCAACATGCTTACAGGAGAGAAAACGCGTGCATGCCATTGG 465  
 QY 361 TGAAGTAAGGTGTGATACGATCGTCCCTTATTAGGAGGCAACAGACGGTCTGACATGA 420  
 Db 466 TGAAGTAAGGTGTGATACGATCGTCCCTTATTAGGAGGCAACAGACGGTCTGACATGA 525  
 QY 421 TTGAGCAACCACTAATTCGCGATTGCAGAGATATTGTATTAAAGTCCTAGCTCGAT 479  
 Db 526 TTGAGCAACCACTAATTCGCGATTGCAGAGATATTGTATTAAAGTCCTAGCTCGAT 585  
 QY 480 ACAATAAGCGCATTCACCATTCACCATTCGGTGGACCTC 523  
 Db 586 ACAATAAGCGCATTCACCATTCACCATTCGGTGGACCTC 629

RESULT 23  
 I58322  
 LOCUS 8591 bp DNA linear PAT 07-OCT-1997  
 DEFINITION Sequence 6 from patent US 5652092.  
 ACCESSION I58322  
 VERSION I58322.1 GI:2477560  
 KEYWORDS  
 SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
JOURNAL Patent: US 5652092-A 6 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..8591  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
DB 4716 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGAGTCTGCTTAGGGTTAGGGCTTTGGG 120  
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCGATGAGAGTCTGCTTAGGGTTAGGGCTTTGGG 4835

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
DB 4836 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 4895

QY 181 CGAAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTAGTTGCG 240  
DB 4896 CGAAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTAGTTGCG 4955

QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 4956 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015

QY 301 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGG 360  
DB 5016 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGG 5075

QY 361 TGGAGTAAGGTGGTACATCGTGCCTTATAGGAGGCAACAGCGGTCTGCATGGA 420  
DB 5076 TGGAGTAAGGTGGTACATCGTGCCTTATAGGAGGCAACAGCGGTCTGCATGGA 5135

QY 421 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
DB 5136 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 5195

QY 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGAGAGTCTGCTTAGGGTTAGGGCTTTGGG 120  
DB 5196 ACAATAAGCCATTGACCAATTCACCAATTCGATGAGAGTCTGCTTAGGGTTAGGGCTTTGGG 120

RESULT 24  
I58323  
LOCUS I58323 8591 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 8 from patent US 5652092.  
ACCESSION I58323  
VERSION I58323.1 GI:2477561  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
JOURNAL Patent: US 5652092-A 8 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..8591  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
DB 4716 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGAGTCTGCTTAGGGTTAGGGCTTTGGG 120  
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCGATGAGAGTCTGCTTAGGGTTAGGGCTTTGGG 4835

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
DB 4836 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 4895

QY 181 CGAAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTAGTTGCG 240  
DB 4896 CGAAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCTCAGGATATAGTAGTTGCG 4955

QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 4956 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015

QY 301 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGG 360  
DB 5016 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGG 5075

QY 361 TGGAGTAAGGTGGTACATCGTGCCTTATAGGAGGCAACAGCGGTCTGCATGGA 420  
DB 5076 TGGAGTAAGGTGGTACATCGTGCCTTATAGGAGGCAACAGCGGTCTGCATGGA 5135

QY 421 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
DB 5136 TTGGACCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 5195

QY 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGAGAGTCTGCTTAGGGTTAGGGCTTTGGG 120  
DB 5196 ACAATAAGCCATTGACCAATTCACCAATTCGATGAGAGTCTGCTTAGGGTTAGGGCTTTGGG 120

RESULT 25  
I60508  
LOCUS I60508 8591 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 6 from patent US 5656477.  
ACCESSION I60508  
VERSION I60508.1 GI:2478953  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
JOURNAL Patent: US 5656477-A 6 12-AUG-1997;  
FEATURES Location/Qualifiers  
source 1..8591  
/organism="unknown"  
/mol\_type="unassigned DNA"

```

Db 4776 ACAAGGCAAGGCTTGACACAAATGTCATGAAGAATCTGCTTAGGTTAGGCGTTTTCG 4835
Qy 121 CTGCTTCGCATGTACGGCCAGATATTCGCTATCTAGGGGACTAGGGTGTGTTAGG 180
Db 4836 CTGCTTCGCATGTACGGCCAGATATACCGTATCTAGGGGACTAGGGTGTGTTAGG 4895
Qy 181 CGAAAAGCGGGCTTCGGTTGTACCGGTTTAGGAGTCCCTCAGGATATAGTATTGCG 240
Db 4896 CGAAAAGCGGGCTTCGGTTGTACCGGTTTAGGAGTCCCTCAGGATATAGTATTGCG 4955
Qy 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 300
Db 4956 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 5015
Qy 301 TAAAGATAGTATAGCAACATGCTTACAGGAGAGAAAAGCACCCTGTCATGCGATTGG 360
Db 5016 TAAAGATAGTATAGCAACATGCTTACAGGAGAGAAAAGCACCCTGTCATGCGATTGG 5075
Qy 361 TGGAAATAGGTGCTACGATCGCTTATAGGAGGCAACAGACGGGCTGCAATGGA 420
Db 5076 TGGAAATAGGTGCTACGATCGCTTATAGGAGGCAACAGACGGGCTGCAATGGA 5135
Qy 421 TTGGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT 479
Db 5136 TTGGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT 5195
Qy 480 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 523
Db 5196 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 5239

RESULT 26
I60509
LOCUS 8591 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5656477.
ACCESSION I60509
VERSION I60509.1 GI:2478954
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
TITLE Amyloid precursor proteins and method of using same to assess
agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL Patent: US 5656477-A 8 12-AUG-1997;
FEATURES
source
1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 96.7%; Score 505.6; DB 6; Length 8591;
Best Local Similarity 99.0%; Pred. No. 6.7e-143;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db 4716 CTGCTCCCTGCTGTGTGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 4775

Qy 61 ACAGGCAAGGCTTGACGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTCG 120
Db 4776 ACAGGCAAGGCTTGACGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTCG 4835

Qy 121 CTGCTTCGCATGTACGGCCAGATATTCGCTATCTAGGGGACTAGGGTGTGTTAGG 180
Db 4836 CTGCTTCGCATGTACGGCCAGATATTCGCTATCTAGGGGACTAGGGTGTGTTAGG 4895

Qy 181 CGAAAAGCGGGCTTCGGTTGTACCGGTTTAGGAGTCCCTCAGGATATAGTATTGCG 240
Db 4896 CGAAAAGCGGGCTTCGGTTGTACCGGTTTAGGAGTCCCTCAGGATATAGTATTGCG 4955

Qy 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 300
Db 4956 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 5015

Qy 301 TAAAGATAGTATAGCAACATGCTTACAGGAGAGAAAAGCACCCTGTCATGCGATTGG 360
Db 5016 TAAAGATAGTATAGCAACATGCTTACAGGAGAGAAAAGCACCCTGTCATGCGATTGG 5075

Qy 361 TGGAAATAGGTGCTACGATCGCTTATAGGAGGCAACAGACGGGCTGCAATGGA 420
Db 5076 TGGAAATAGGTGCTACGATCGCTTATAGGAGGCAACAGACGGGCTGCAATGGA 5135

Qy 421 TTGGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT 479
Db 5136 TTGGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT 5195

Qy 480 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 523
Db 5196 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 5239

```

```

Qy 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 300
Db 4956 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 5015
Qy 301 TAAAGATAGTATAGCAACATGCTTACAGGAGAGAAAAGCACCCTGTCATGCGATTGG 360
Db 5016 TAAAGATAGTATAGCAACATGCTTACAGGAGAGAAAAGCACCCTGTCATGCGATTGG 5075
Qy 361 TGGAAATAGGTGCTACGATCGCTTATAGGAGGCAACAGACGGGCTGCAATGGA 420
Db 5076 TGGAAATAGGTGCTACGATCGCTTATAGGAGGCAACAGACGGGCTGCAATGGA 5135
Qy 421 TTGGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT 479
Db 5136 TTGGACGAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT 5195
Qy 480 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 523
Db 5196 ACAATAAGCCCATTTGACCATTCACACATTTGGTGTGCACCTC 5239

RESULT 27
I77052
LOCUS 8591 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 6 from patent US 5693478.
ACCESSION I77052
VERSION I77052.1 GI:3013206
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
TITLE Method of detecting amyloid precursor proteins
JOURNAL Patent: US 5693478-A 6 02-DEC-1997;
FEATURES
source
1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 96.7%; Score 505.6; DB 6; Length 8591;
Best Local Similarity 99.0%; Pred. No. 6.7e-143;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db 4716 CTGCTCCCTGCTGTGTGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 4775

Qy 61 ACAGGCAAGGCTTGACGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTCG 120
Db 4776 ACAGGCAAGGCTTGACGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTCG 4835

Qy 121 CTGCTTCGCATGTACGGCCAGATATTCGCTATCTAGGGGACTAGGGTGTGTTAGG 180
Db 4836 CTGCTTCGCATGTACGGCCAGATATTCGCTATCTAGGGGACTAGGGTGTGTTAGG 4895

Qy 181 CGAAAAGCGGGCTTCGGTTGTACCGGTTTAGGAGTCCCTCAGGATATAGTATTGCG 240
Db 4896 CGAAAAGCGGGCTTCGGTTGTACCGGTTTAGGAGTCCCTCAGGATATAGTATTGCG 4955

Qy 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 300
Db 4956 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 5015

Qy 301 TAAAGATAGTATAGCAACATGCTTACAGGAGAGAAAAGCACCCTGTCATGCGATTGG 360
Db 5016 TAAAGATAGTATAGCAACATGCTTACAGGAGAGAAAAGCACCCTGTCATGCGATTGG 5075

Qy 361 TGGAAATAGGTGCTACGATCGCTTATAGGAGGCAACAGACGGGCTGCAATGGA 420
Db 5076 TGGAAATAGGTGCTACGATCGCTTATAGGAGGCAACAGACGGGCTGCAATGGA 5135

```

QY 421 TTGGACGACCACTAATTCGCGATTCAGAGAT-ATTGTATTAAAGTCTAGCTCGAT 479  
Db 5136 TTGGACGACCACTAATTCGCGATTCAGAGAT-ATTGTATTAAAGTCTAGCTCGAT 5195

QY 480 ACAATAAAGCCATTGACCAATTCACCAATTCGTTGTCACCTC 523  
Db 5196 ACAATAAAGCCATTGACCAATTCACCAATTCGTTGTCACCTC 5239

RESULT 28  
LOCUS I77053  
DEFINITION Sequence 8 from patent US 5693478.  
ACCESSION I77053  
VERSION I77053.1 GI:3013207  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Method of detecting amyloid precursor proteins  
JOURNAL Patent: US 5693478-A 8 02-DEC-1997;  
FEATURES Location/Qualifiers  
source 1..8591  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAAGTATTCGATGAGGAGTAAAGTCTA 60  
Db 4716 CTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAAGTATTCGATGAGGAGTAAAGTCTA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGCTAGGTTAGGCGTTTTCG 120  
Db 4776 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGCTAGGTTAGGCGTTTTCG 4835

QY 121 CTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAAGTATTCGATGAGGAGTAAAGTCTA 180  
Db 4836 CTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAAGTATTCGATGAGGAGTAAAGTCTA 4895

QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTCGC 240  
Db 4896 CGAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTCGC 4955

QY 241 TTTTGCATAGGAGGAGGAGAAATGATCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGCATAGGAGGAGGAGAAATGATCTTATGCAATCTCTGTAGTCTTGCACATGG 5015

QY 301 TAAAGATGATTAGCAATCATGCTTACAGGAGAGAAAAAGCACCGTGCATGCCGATTGG 360  
Db 5016 TAAAGATGATTAGCAATCATGCTTACAGGAGAGAAAAAGCACCGTGCATGCCGATTGG 5075

QY 361 TGGAGTATAGGTGTGATCGATCGTCCCTTATAGAGGAGCAACAGAGGCTCTGACATGA 420  
Db 5076 TGGAGTATAGGTGTGATCGATCGTCCCTTATAGAGGAGCAACAGAGGCTCTGACATGA 5135

QY 421 TTGGACGACCACTAATTCGCGATTCAGAGAT-ATTGTATTAAAGTCTAGCTCGAT 479  
Db 5136 TTGGACGACCACTAATTCGCGATTCAGAGAT-ATTGTATTAAAGTCTAGCTCGAT 5195

QY 480 ACAATAAAGCCATTGACCAATTCACCAATTCGTTGTCACCTC 523  
Db 5196 ACAATAAAGCCATTGACCAATTCACCAATTCGTTGTCACCTC 5239

RESULT 29  
LOCUS I87173  
DEFINITION Sequence 8 from patent US 5703209.  
ACCESSION I87173  
VERSION I87173.1 GI:3206892  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide

DEFINITION Sequence 6 from patent US 5703209.  
ACCESSION I87173  
VERSION I87173.1 GI:3206891  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide  
JOURNAL Patent: US 5703209-A 6 30-DEC-1997;  
FEATURES Location/Qualifiers  
source 1..8591  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAAGTATTCGATGAGGAGTAAAGTCTA 60  
Db 4716 CTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAAGTATTCGATGAGGAGTAAAGTCTA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGCTAGGTTAGGCGTTTTCG 120  
Db 4776 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGCTAGGTTAGGCGTTTTCG 4835

QY 121 CTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAAGTATTCGATGAGGAGTAAAGTCTA 180  
Db 4836 CTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAAGTATTCGATGAGGAGTAAAGTCTA 4895

QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTCGC 240  
Db 4896 CGAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTCGC 4955

QY 241 TTTTGCATAGGAGGAGGAGAAATGATCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGCATAGGAGGAGGAGAAATGATCTTATGCAATCTCTGTAGTCTTGCACATGG 5015

QY 301 TAAAGATGATTAGCAATCATGCTTACAGGAGAGAAAAAGCACCGTGCATGCCGATTGG 360  
Db 5016 TAAAGATGATTAGCAATCATGCTTACAGGAGAGAAAAAGCACCGTGCATGCCGATTGG 5075

QY 361 TGGAGTATAGGTGTGATCGATCGTCCCTTATAGAGGAGCAACAGAGGCTCTGACATGA 420  
Db 5076 TGGAGTATAGGTGTGATCGATCGTCCCTTATAGAGGAGCAACAGAGGCTCTGACATGA 5135

QY 421 TTGGACGACCACTAATTCGCGATTCAGAGAT-ATTGTATTAAAGTCTAGCTCGAT 479  
Db 5136 TTGGACGACCACTAATTCGCGATTCAGAGAT-ATTGTATTAAAGTCTAGCTCGAT 5195

QY 480 ACAATAAAGCCATTGACCAATTCACCAATTCGTTGTCACCTC 523  
Db 5196 ACAATAAAGCCATTGACCAATTCACCAATTCGTTGTCACCTC 5239

RESULT 30  
LOCUS I87174  
DEFINITION Sequence 8 from patent US 5703209.  
ACCESSION I87174  
VERSION I87174.1 GI:3206892  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 8591)  
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.  
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide

JOURNAL Patent: US 5703209-A 8 30-DEC-1997;

# FEATURES

source  
Location/Qualifiers  
1. .8591  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 96.7%; Score 505.6; DB 6; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTTGAGGTGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
DB 4716 CTGCTCCCTGCTGTGTTGAGGTGCTGAGTAGTGCAGCAAAATTTAAGCTACA 4775

QY 61 ACAAGGCAAGGCTTACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGTTTTCGG 120  
DB 4776 ACAAGGCAAGGCTTACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGTTTTCGG 4835

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTTTCGG 180  
DB 4836 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTTTCGG 4895

QY 181 CGAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
DB 4896 CGAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 4955

QY 241 TTTTGCATAGGAGGGGAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 300  
DB 4956 TTTTGCATAGGAGGGGAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 5015

QY 301 TAAAGCATGATGATGACCAATGCTCTTACAGGAGAGAAAGACCTGTCGCGATTGG 360  
DB 5016 TAAAGCATGATGATGACCAATGCTCTTACAGGAGAGAAAGACCTGTCGCGATTGG 5075

QY 361 TGAAGTAAAGTGTGATGATGCTGCTTATAGGAAGCAACAGCGGTCTGATGGA 420  
DB 5076 TGAAGTAAAGTGTGATGATGCTGCTTATAGGAAGCAACAGCGGTCTGATGGA 5135

QY 421 TTGAGCAACCACTAATTCGATTCGAGAGAT-ATTGTATTATAGTCCCTAGCTCGAT 479  
DB 5136 TTGAGCAACCACTAATTCGATTCGAGAGAT-ATTGTATTATAGTCCCTAGCTCGAT 5195

QY 480 ACAATAAGCCATTGACCAATTCACACATTTGGTGTGCACCTC 523  
DB 5196 ACAATAAGCCATTGACCAATTCACACATTTGGTGTGCACCTC 5239

## RESULT 31

XXU02428 10737 bp DNA circular SYN 29-JAN-1997  
LOCUS Cloning vector pBR2, complete sequence.  
DEFINITION U02428  
ACCESSION U02428  
VERSION U02428.1 GI:413794

Cloning vector pBR2

Cloning vector pBR2

artificial sequences; vectors.

1. (bases 1 to 10737)

Murphy, A.J., Kung, A.L., Swirski, R.A. and Schimke, R.T.

cDNA expression cloning in human cells using the pBR2

episonal vector system

Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)

2. (bases 1 to 10737)

Kitts, P.A.

ClonTECH Vectors On Disc version 1.3

Unpublished

3. (bases 1 to 10737)

Kitts, P.A.

Direct Submission

Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,

1020 East Meadow Circle, Palo Alto, CA 94303, USA

This vector can be obtained from CLONTECH Laboratories, Inc., 1020

COMMENT

East Meadow Circle, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424-8222 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH; this vector has not been completely sequenced. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.

## FEATURES

source  
Location/Qualifiers  
1. .10737  
/organism="Cloning vector pBR2"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31805"

## ORIGIN

Query Match 96.7%; Score 505.6; DB 12; Length 10737;  
Best Local Similarity 99.0%; Pred. No. 6.7e-143;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTTGAGGTGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
DB 148 CTGCTCCCTGCTGTGTTGAGGTGCTGAGTAGTGCAGCAAAATTTAAGCTACA 207

QY 61 ACAAGGCAAGGCTTACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGTTTTCGG 120  
DB 208 ACAAGGCAAGGCTTACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGTTTTCGG 267

QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTTTCGG 180  
DB 268 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTTTCGG 327

QY 181 CGAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
DB 328 CGAAAGCGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 387

QY 241 TTTTGCATAGGAGGGGAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 300  
DB 388 TTTTGCATAGGAGGGGAATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGG 447

QY 301 TAAAGCATGATGATGACCAATGCTCTTACAGGAGAGAAAGACCTGTCGCGATTGG 360  
DB 448 TAAAGCATGATGATGACCAATGCTCTTACAGGAGAGAAAGACCTGTCGCGATTGG 507

QY 361 TGAAGTAAAGTGTGATGATGCTGCTTATAGGAAGCAACAGCGGTCTGATGGA 420  
DB 508 TGAAGTAAAGTGTGATGATGCTGCTTATAGGAAGCAACAGCGGTCTGATGGA 567

QY 421 TTGAGCAACCACTAATTCGATTCGAGAGAT-ATTGTATTATAGTCCCTAGCTCGAT 479  
DB 568 TTGAGCAACCACTAATTCGATTCGAGAGAT-ATTGTATTATAGTCCCTAGCTCGAT 627

QY 480 ACAATAAGCCATTGACCAATTCACACATTTGGTGTGCACCTC 523  
DB 628 ACAATAAGCCATTGACCAATTCACACATTTGGTGTGCACCTC 671

## RESULT 32

U02455 10850 bp DNA circular SYN 29-MAR-1996  
LOCUS Cloning vector rpBR2, complete sequence.  
DEFINITION U02455  
ACCESSION U02455  
VERSION U02455.1 GI:413821

Cloning vector rpBR2

Cloning vector rpBR2

artificial sequences; vectors.

1. (bases 1 to 10850)

Kitts, P.A.

CLONTECH Vectors On Disc version 1.3

Unpublished

JOURNAL

```

REFERENCE 2 (bases 1 to 10850)
AUTHORS Murphy,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
TITLE cDNA expression cloning in human cells using the plambdADR2
episomal vector system
JOURNAL Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)
REFERENCE 3 (bases 1 to 10850)
AUTHORS Kitts,P.A.
JOURNAL Direct Submission
TITLE Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT Lambda DR2 can be obtained from CLONTECH Laboratories, Inc., 1020
East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
call (415) 424-8222 or (800) 662-2566, extension 1. International
customers, please contact your local distributor. For technical
information, call (415) 424-8222 or (800) 662-2566, extension 3.
This sequence was compiled by Andrew Murphy and revised at
CLONTECH. If you suspect there is an error in this sequence, please
contact CLONTECH's technical Service Department at (415) 424-8222
or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.

FEATURES
source
1..10850
/organism="Cloning vector rpDR2"
/mol_type="genomic DNA"
/db_xref="taxon:31858"
/note="Plasmid released from lambda DR2"

ORIGIN
Query Match 96.7%; Score 505.6; DB 12; Length 10850;
Best Local Similarity 99.0%; Pred. No. 6.7e-143;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60
Db 148 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 207
QY 61 ACAAGCAGGCTTGCACGACATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 120
Db 208 ACAAGCAGGCTTGCACGACATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 267
QY 121 CTGCTTCGGATGTACGGGCGAGATTCGCGTATCTGAGGGGACTAGGTTGTTAGG 180
Db 268 CTGCTTCGGATGTACGGGCGAGATTCGCGTATCTGAGGGGACTAGGTTGTTAGG 327
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 240
Db 328 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 387
QY 241 TTTTGCATAGGGGGGGAATGTAGTCTTATGCAATCTCTGTAGCTTGCACATGG 300
Db 388 TTTTGCATAGGGGGGGAATGTAGTCTTATGCAATCTCTGTAGCTTGCACATGG 447
QY 301 TAACGATGAGTTAGCAATGCTTACAAGGAGAGAAAAGCACCGTGCAATGCCGATTGG 360
Db 448 TAACGATGAGTTAGCAATGCTTACAAGGAGAGAAAAGCACCGTGCAATGCCGATTGG 507
QY 361 TGAAGTAAAGTGTGATGATCGTGGCTTATTAGAGAGGCAACAGACGGGTCTGACATGA 420
Db 508 TGAAGTAAAGTGTGATGATCGTGGCTTATTAGAGAGGCAACAGACAGGTCTGACATGA 567
QY 421 TTGAGCGAACCACTAAATTCGCGATTTCGAGAGAT-ATTGTATTTAAGTGTGCTAGCTCGAT 479
Db 568 TTGAGCGAACCACTAAATTCGCGATTTCGAGAGATTTATTTAAGTGTGCTAGCTCGAT 627
QY 480 ACAATAAGCGCCATTGACCAATTCACCACATTGGTGTGCACCTC 523
Db 628 ACAATAAGCGCCATTGACCAATTCACCACATTGGTGTGCACCTC 671

RESULT 33
ALAPROLTB
LOCUS 633 bp ss-RNA linear VRL 28-APR-1993
DEFINITION Rous sarcoma virus (Schmidt-Ruppin), proviral, 3' LTR on 21S mRNA.
ACCESSION J02025 J02022

```

```

J02025.1 GI:210255
c-myc proto-oncogene; long terminal repeat (LTR); src oncogene.
Rous sarcoma virus
Rous sarcoma virus
Viruses; Retroviridae; Retroviridae; Alpharetrovirus.
REFERENCE 1 (sites)
AUTHORS Yamamoto,T., de Crombrughe,B. and Pastan,I.
TITLE Identification of a functional promoter in the long terminal repeat
of Rous sarcoma virus
JOURNAL Cell 22 (3), 787-797 (1980)
MEDLINE 81112147
PUBMED 6257399
REFERENCE 2 (bases 1 to 633)
AUTHORS Yamamoto,T., Tyagi,J.S., Pagan,J.B., Jay,G., deCrombrughe,B. and
Pastan,I.
TITLE Molecular mechanism for the capture and excision of the
transforming gene of avian sarcoma virus as suggested by analysis
of recombinant clones
J. Virol. 35 (2), 436-443 (1980)
MEDLINE 81072438
PUBMED 6255184
REFERENCE 3 (bases 319 to 633)
AUTHORS Yamamoto,T., Jay,G. and Pastan,I.
TITLE Unusual features in the nucleotide sequence of a cDNA clone derived
from the common region of avian sarcoma virus messenger RNA
Proc. Natl. Acad. Sci. U.S.A. 77 (1), 176-180 (1980)
MEDLINE 80145590
PUBMED 6244542
COMMENT Original source text: Rous sarcoma virus (Schmidt-Ruppin strain,
subgroup D) provirus, cDNA to 21S mRNA from infected chicken
embryonic fibroblasts, clone pSR1.
[1] sites; mRNA start.
Original figure in [2] included 24 'g's on 5' end and 16 'c's on 3'
end that were cDNA synthesis artifacts.
[2] also sequenced a defective clone, pSR2, with the src gene
deleted (see separate entry).
[1] demonstrated the mRNA transcription initiation site shown in
the Sites table using pSR1 as a template. However, this is the 3'
LTR, and the functional mRNA start site would be assumed to be on
the 5' LTR at the homologous site.

FEATURES
source
1..633
/organism="Rous sarcoma virus"
/mol_type="genomic RNA"
/db_xref="taxon:11886"
<1..517
/note="viral genomic RNA"
211..633
/note="3' LTR"
517..633
/note="in vitro mRNA [1]; see comment"
repeat_region 517..636
/note="terminally redundant repeat"
ORIGIN 20 bp upstream of pSR1 site.

Query Match 96.5%; Score 504.6; DB 14; Length 633;
Best Local Similarity 99.0%; Pred. No. 1.3e-142;
Matches 518; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60
Db 28 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 87
QY 61 ACAAGCAAGGCTTGACCGACATTCGATGAGAAATCTGCTTAGGTTAGCGTTTTCGG 120
Db 88 ACAAGCAAGGCTTGACCGACATTCGATGAGAAATCTGCTTAGGTTAGCGTTTTCGG 147
QY 121 CTGCTTCGGATGTACGGGCGAGATTCGCGTATCTGAGGGGACTAGGTTGTTAGG 180
Db 148 CTGCTTCGGATGTACGGGCGAGATTCGCGTATCTGAGGGGACTAGGTTGTTAGG 207
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 240

```

Db 208 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGAGATATAGTAGTTTCG 267  
Qy 241 TTTTGCATAGGAGGAGGGAATAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Db 268 TTTTGCATAGGAGGAGGGAATAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 327  
Qy 301 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATGG 360  
Db 328 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATGG 387  
Qy 361 TGGAGTAAGGTGGTACGATCGTCTTATAGGAGGAGCAACAGCGGTCTGCATGGA 420  
Db 388 TGGAGTAAGGTGGTACGATCGTCTTATAGGAGGAGCAACAGCGGTCTGCATGGA 447  
Qy 421 TTGACGAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 448 TTGACGAACCACTGAATTCGCAATTCGAGATTAATGTATTAAAGTGCCTAGCTCGAT 507  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGGTGCACCT 522  
Db 508 ACAATAAGCCATTGACCAATTCACCAATTCGATGGTGCACCT 550

RESULT 34  
AR215114  
LOCUS AR215114 6836 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 18 from patent US 6410266.  
ACCESSION AR215114  
VERSION AR215114.1 GI:23313242  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6836)  
AUTHORS Harrington,J.J. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6410266-A 18 25-JUN-2002;  
FEATURES Location/Qualifiers  
source 1..6836  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 1358  
Qy 61 ACAAGGCAAGGCTTGACGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 120  
Db 1359 ACAAGGCAAGGCTTGACGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 1418  
Qy 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 180  
Db 1419 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 1478  
Qy 181 CGAAAGCGGGCTTCGGTTGTACGGGTAGGATCCCTCAGGATATAGTATTTCG 240  
Db 1299 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 1358  
Qy 61 ACAAGGCAAGGCTTGACGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 120  
Db 1359 ACAAGGCAAGGCTTGACGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 1418  
Qy 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 180  
Db 1419 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 1478  
Qy 181 CGAAAGCGGGCTTCGGTTGTACGGGTAGGATCCCTCAGGATATAGTATTTCG 240  
Db 1479 CGCCACGCGGGCTTCGGTTGTACGGGTAGGATCCCTCAGGATATAGTATTTCG 1538  
Qy 241 TTTTGCATAGGAGGAGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Db 1539 TTTTGCATAGGAGGAGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1598  
Qy 301 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATGG 360  
Db 1599 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATGG 1658  
Qy 361 TGGAGTAAGGTGGTACGATCGTCTTATAGGAGGAGCAACAGCGGTCTGCATGGA 420  
Db 1659 TGGAGTAAGGTGGTACGATCGTCTTATAGGAGGAGCAACAGCGGTCTGCATGGA 1718  
Qy 421 TTGACGAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1719 TTGACGAACCACTGAATTCGCAATTCGAGATTAATGTATTAAAGTGCCTAGCTCGAT 1778  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGGTGCACCT 522  
Db 1779 ACAATAAGCCATTGACCAATTCACCAATTCGATGGTGCACCT 1822

Db 1659 TGGAGTAAGGTGGTACGATCGTCTTATAGGAGGAGCAACAGCGGTCTGCATGGA 1718  
Qy 421 TTGACGAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1719 TTGACGAACCACTGAATTCGCAATTCGAGATTAATGTATTAAAGTGCCTAGCTCGAT 1778  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGGTGCACCT 522  
Db 1779 ACAATAAGCCATTGACCAATTCACCAATTCGATGGTGCACCT 1822

RESULT 35  
AR302356  
LOCUS AR302356 6836 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 18 from patent US 6541221.  
ACCESSION AR302356  
VERSION AR302356.1 GI:31690610  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6836)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 18 01-APR-2003;  
FEATURES Location/Qualifiers  
source 1..6836  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 1358  
Qy 61 ACAAGGCAAGGCTTGACGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 120  
Db 1359 ACAAGGCAAGGCTTGACGCAATTCGATGAAGATCTGTTAGGTTAGGCTTTTTCG 1418  
Qy 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 180  
Db 1419 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTCAGGGGACTAGGCTGTGTTAGG 1478  
Qy 181 CGAAAGCGGGCTTCGGTTGTACGGGTAGGATCCCTCAGGATATAGTATTTCG 240  
Db 1479 CGCCACGCGGGCTTCGGTTGTACGGGTAGGATCCCTCAGGATATAGTATTTCG 1538  
Qy 241 TTTTGCATAGGAGGAGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Db 1539 TTTTGCATAGGAGGAGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1598  
Qy 301 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATGG 360  
Db 1599 TAACGATGAGTTAGCAACATGCCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATGG 1658  
Qy 361 TGGAGTAAGGTGGTACGATCGTCTTATAGGAGGAGCAACAGCGGTCTGCATGGA 420  
Db 1659 TGGAGTAAGGTGGTACGATCGTCTTATAGGAGGAGCAACAGCGGTCTGCATGGA 1718  
Qy 421 TTGACGAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1719 TTGACGAACCACTGAATTCGCAATTCGAGATTAATGTATTAAAGTGCCTAGCTCGAT 1778  
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGGTGCACCT 522  
Db 1779 ACAATAAGCCATTGACCAATTCACCAATTCGATGGTGCACCT 1822



RESULT 36  
 AR373228  
 LOCUS AR373228 6836 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 18 from patent US 6602686.  
 ACCESSION AR373228  
 VERSION AR373228.1 GI:40075236  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 6836)  
 AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
 TITLE Compositions and method for non-targeted activation of endogenous genes  
 JOURNAL Patent: US 6602686-A 18 05-AUG-2003;  
 FEATURES Location/Qualifiers  
 source 1..6836  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 95.8%; Score 500.8; DB 6; Length 6836;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 1 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 1299 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 1358  
 Qy 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCGC 120  
 Db 1359 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCGC 1418  
 Qy 121 CTGCTTCGCGATGACCGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180  
 Db 1419 CTGCTTCGCGATGACCGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 1478  
 Qy 181 CGAAAGCGGGGCTTCGCTGCTACGGGTTAGGAGTCCCTCAGGATATAGTACTTTCGC 240  
 Db 1479 CGCCAGCGGGGCTTCGCTGCTACGGGTTAGGAGTCCCTCAGGATATAGTACTTTCGC 1538  
 Qy 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 300  
 Db 1539 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 1598  
 Qy 301 TAACGATGATGACCAATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATGG 360  
 Db 1599 TAACGATGATGACCAATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATGG 1658  
 Qy 361 TGGAGTAAAGTGGTACGATCGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 420  
 Db 1659 TGGAGTAAAGTGGTACGATCGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 1718  
 Qy 421 TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
 Db 1719 TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1778  
 Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 1779 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1822

RESULT 37  
 AR401614  
 LOCUS AR401614 6836 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 18 from patent US 6623956.  
 ACCESSION AR401614  
 VERSION AR401614.1 GI:40149062  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 6836)  
 AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
 TITLE Compositions and methods for non-targeted activation of endogenous genes  
 JOURNAL Patent: US 6623956-A 18 23-SEP-2003;  
 FEATURES Location/Qualifiers  
 source 1..6836  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 95.8%; Score 500.8; DB 6; Length 6836;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 1 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 1299 CTGCTCCCTGCTTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 1358  
 Qy 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCGC 120  
 Db 1359 ACAAGCAAGGCTTGACCGCAATTCATGAAGATCTGCTTAGGGTTAGGCGTTTTCGC 1418  
 Qy 121 CTGCTTCGCGATGACCGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180  
 Db 1419 CTGCTTCGCGATGACCGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 1478  
 Qy 181 CGAAAGCGGGGCTTCGCTGCTACGGGTTAGGAGTCCCTCAGGATATAGTACTTTCGC 240  
 Db 1479 CGCCAGCGGGGCTTCGCTGCTACGGGTTAGGAGTCCCTCAGGATATAGTACTTTCGC 1538  
 Qy 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 300  
 Db 1539 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 1598  
 Qy 301 TAACGATGATGACCAATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATGG 360  
 Db 1599 TAACGATGATGACCAATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATGG 1658  
 Qy 361 TGGAGTAAAGTGGTACGATCGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 420  
 Db 1659 TGGAGTAAAGTGGTACGATCGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 1718  
 Qy 421 TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
 Db 1719 TTGAGCAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1778  
 Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 1779 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1822

RESULT 38  
 AF346624  
 LOCUS AF346624 6836 bp DNA circular SYN 30-AUG-2001  
 DEFINITION RAGE vector pRIGI, complete sequence.  
 ACCESSION AF346624  
 VERSION AF346624.1 GI:15383987  
 KEYWORDS  
 SOURCE RAGE vector pRIGI  
 ORGANISM RAGE vector pRIGI  
 1 (bases 1 to 6836)  
 artificial sequences; vectors.  
 REFERENCE 1 (bases 1 to 6836)  
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,  
 Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boorer,S.,  
 Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,  
 Offenbacher,J., Danzig,J. and Ducar,M.  
 TITLE Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
 MEDLINE 21227151  
 PUBMED 11329013

```
REFERENCE 2 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Velo,N., Hess,J., Cochran,K., Io,K., Offenbacher,J., Danzig,J.,
and Ducat,M.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2001) Athersys, Inc., 3201 Carnegie Ave.,
Cleveland, OH 44115, USA
FEATURES
source 1. 6836
Location/Qualifiers
/organism="RAGE vector pRIG1"
/mol_type="genomic DNA"
/db_xref="taxon:161236"
ORIGIN
Query Match 95.8%; Score 500.8; DB 12; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.9e-141;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
Qy 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 60
Db CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 1358
Qy 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGCAGGAGCAAAATTAAGCTACA 120
Db ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGCAGGAGCAAAATTAAGCTACA 1418
Qy 121 CTGCTCCGATGTACGGGCGAGATATCGGATATCTGAGGGACTAGGGTGTGTAGG 180
Db CTGCTCCGATGTACGGGCGAGATATCGGATATCTGAGGGACTAGGGTGTGTAGG 1478
Qy 181 CGAAAGCGGGCTTCGGTGTACGGGCTTACGAGTCCCTCAGGATATAGTATTCGC 240
Db CGCCAGCGGGCTTCGGTGTACGGGCTTACGAGTCCCTCAGGATATAGTATTCGC 1538
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 300
Db TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 1598
Qy 301 TAACGATGAGTACCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 360
Db TAACGATGAGTACCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 1658
Qy 361 TGGAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 420
Db TGGAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 1718
Qy 421 TTGGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479
Db TTGGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1778
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523
Db ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1822
RESULT 39
AR215118
LOCUS 9737 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 22 from patent US 6410266.
ACCESSION AR215118
VERSION AR215118.1 GI:23313246
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 22 25-JUN-2002;
FEATURES
source 1. 9737
Location/Qualifiers
/organism="genomic DNA"
/db_xref="taxon:161236"
ORIGIN
Query Match 95.8%; Score 500.8; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-141;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
Qy 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 60
Db CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 1211
Qy 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGCAGGAGCAAAATTAAGCTACA 120
Db ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGCAGGAGCAAAATTAAGCTACA 1271
Qy 121 CTGCTCCGATGTACGGGCGAGATATCGGATATCTGAGGGACTAGGGTGTGTAGG 180
Db CTGCTCCGATGTACGGGCGAGATATCGGATATCTGAGGGACTAGGGTGTGTAGG 1391
Qy 181 CGAAAGCGGGCTTCGGTGTACGGGCTTACGAGTCCCTCAGGATATAGTATTCGC 240
Db CGCCAGCGGGCTTCGGTGTACGGGCTTACGAGTCCCTCAGGATATAGTATTCGC 1391
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 300
Db TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 1451
Qy 301 TAACGATGAGTACCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 360
Db TAACGATGAGTACCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 1511
Qy 361 TGGAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 420
Db TGGAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 1571
Qy 421 TTGGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479
Db TTGGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523
Db ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1675
RESULT 40
AR215119
LOCUS 9737 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 23 from patent US 6410266.
ACCESSION AR215119
VERSION AR215119.1 GI:23313247
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 23 25-JUN-2002;
FEATURES
source 1. 9737
Location/Qualifiers
/organism="genomic DNA"
/db_xref="taxon:161236"
ORIGIN
Query Match 95.8%; Score 500.8; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-141;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
Qy 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 60
Db CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTACA 1211
Qy 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGCAGGAGCAAAATTAAGCTACA 120
Db ACAAGGCAAGGCTTGACCGCAATTCGATGAGTGCAGGAGCAAAATTAAGCTACA 1271
Qy 121 CTGCTCCGATGTACGGGCGAGATATCGGATATCTGAGGGACTAGGGTGTGTAGG 180
Db CTGCTCCGATGTACGGGCGAGATATCGGATATCTGAGGGACTAGGGTGTGTAGG 1391
Qy 181 CGAAAGCGGGCTTCGGTGTACGGGCTTACGAGTCCCTCAGGATATAGTATTCGC 240
Db CGCCAGCGGGCTTCGGTGTACGGGCTTACGAGTCCCTCAGGATATAGTATTCGC 1391
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 300
Db TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGG 1451
Qy 301 TAACGATGAGTACCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 360
Db TAACGATGAGTACCAATCGCTTACAGGAGGAGAAAGACCGTGCATGCCGATTGG 1511
Qy 361 TGGAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 420
Db TGGAGTAAAGTGTGACATCGTGCCTTATAGGAGGCAACAGACGGTCTGACATGGA 1571
Qy 421 TTGGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479
Db TTGGACGACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631
Qy 480 ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523
Db ACAATAAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 1675
```

Db 1152 CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 1211  
Qy 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGCTTAGCGCTTTTGGC 120  
Db 1212 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGCTTAGCGCTTTTGGC 1271  
Qy 121 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGGTGTATTAGG 180  
Db 1272 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGGTGTATTAGG 1331  
Qy 181 CGAAAGCGGGGCTTCCGCTTGTAGCGGTTAGGATCCCTCAGGATATAGTATTTCGC 240  
Db 1332 CGCCAGCGGGGCTTCCGCTTGTAGCGGTTAGGATCCCTCAGGATATAGTATTTCGC 1391  
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 300  
Db 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 1451  
Qy 301 TAACGATGATTAGCAATGCTCTTACAAGGAGAAAGCAACCGTGATGCCGATGG 360  
Db 1452 TAACGATGATTAGCAATGCTCTTACAAGGAGAAAGCAACCGTGATGCCGATGG 1511  
Qy 361 TGGAGTAAAGTGTACGATCGCTTATTAGGAGGCAACGAGCGGTCTGACATGA 420  
Db 1512 TGGAGTAAAGTGTACGATCGCTTATTAGGAGGCAACGAGCGGTCTGACATGA 1571  
Qy 421 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1572 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631  
Qy 480 ACAATAAGCGCATTTGACATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCGCATTTGACATTCACCAATTTGGTGTGCACCTC 1675

RESULT 41  
AR215124  
LOCUS AR215124 9737 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 28 from patent US 6410266.  
ACCESSION AR215124  
VERSION AR215124.1 GI:23313252  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9737)  
AUTHORS Harrington,J.J. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6410266-A 28 25-JUN-2002;  
FEATURES Location/Qualifiers  
source 1..9737  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 1211  
Qy 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGCTTAGCGCTTTTGGC 120  
Db 1212 CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 1211  
Qy 121 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGGTGTATTAGG 180  
Db 1272 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGGTGTATTAGG 1331  
Qy 181 CGAAAGCGGGGCTTCCGCTTGTAGCGGTTAGGATCCCTCAGGATATAGTATTTCGC 240  
Db 1332 CGCCAGCGGGGCTTCCGCTTGTAGCGGTTAGGATCCCTCAGGATATAGTATTTCGC 1391  
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 300  
Db 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 1451  
Qy 301 TAACGATGATTAGCAATGCTCTTACAAGGAGAAAGCAACCGTGATGCCGATGG 360  
Db 1452 TAACGATGATTAGCAATGCTCTTACAAGGAGAAAGCAACCGTGATGCCGATGG 1511  
Qy 361 TGGAGTAAAGTGTACGATCGCTTATTAGGAGGCAACGAGCGGTCTGACATGA 420  
Db 1512 TGGAGTAAAGTGTACGATCGCTTATTAGGAGGCAACGAGCGGTCTGACATGA 1571  
Qy 421 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1572 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631  
Qy 480 ACAATAAGCGCATTTGACATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCGCATTTGACATTCACCAATTTGGTGTGCACCTC 1675

Db 1332 CGCCAGCGGGGCTTCCGCTTGTAGCGGTTAGGATCCCTCAGGATATAGTATTTCGC 1391  
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 300  
Db 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 1451  
Qy 301 TAACGATGATTAGCAATGCTCTTACAAGGAGAAAGCAACCGTGATGCCGATGG 360  
Db 1452 TAACGATGATTAGCAATGCTCTTACAAGGAGAAAGCAACCGTGATGCCGATGG 1511  
Qy 361 TGGAGTAAAGTGTACGATCGCTTATTAGGAGGCAACGAGCGGTCTGACATGA 420  
Db 1512 TGGAGTAAAGTGTACGATCGCTTATTAGGAGGCAACGAGCGGTCTGACATGA 1571  
Qy 421 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1572 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631  
Qy 480 ACAATAAGCGCATTTGACATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCGCATTTGACATTCACCAATTTGGTGTGCACCTC 1675

RESULT 42  
AR302360  
LOCUS AR302360 9737 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 22 from patent US 6541221.  
ACCESSION AR302360  
VERSION AR302360.1 GI:31690614  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9737)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 22 01-APR-2003;  
FEATURES Location/Qualifiers  
source 1..9737  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACA 1211  
Qy 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGCTTAGCGCTTTTGGC 120  
Db 1212 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGCTTAGCGCTTTTGGC 1271  
Qy 121 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGGTGTATTAGG 180  
Db 1272 CTGCTTCGCGATGTACGCGCCAGATATTCGCGTATCTGAGGGGACTAGGGGTGTATTAGG 1331  
Qy 181 CGAAAGCGGGGCTTCCGCTTGTAGCGGTTAGGATCCCTCAGGATATAGTATTTCGC 240  
Db 1332 CGCCAGCGGGGCTTCCGCTTGTAGCGGTTAGGATCCCTCAGGATATAGTATTTCGC 1391  
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 300  
Db 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 1451  
Qy 301 TAACGATGATTAGCAATGCTCTTACAAGGAGAAAGCAACCGTGATGCCGATGG 360  
Db 1452 TAACGATGATTAGCAATGCTCTTACAAGGAGAAAGCAACCGTGATGCCGATGG 1511

QY 361 TGGAAAGTAAAGTGTGATGATCGTCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420  
Db 1512 TGGAAAGTAAAGTGTGATGATCGTCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1571  
QY 421 TTGAGCAACCACTAAATTCGGATTGCGATGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1572 TTGAGCAACCACTAAATTCGGATTGCGATGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631  
QY 480 ACAATAAGCCCATTTGACCAATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCCCATTTGACCAATTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 43  
AR302361  
LOCUS AR302361 9737 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 23 from patent US 6541221.  
ACCESSION AR302361  
VERSION AR302361.1 GI:31690615  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9737)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 23 01-APR-2003;  
FEATURES Location/Qualifiers  
source 1..9737  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 1211  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTGGC 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTGGC 1271  
QY 121 CTGCTCCGATGTACGGGCCAGATATTCGCGTATCTGAGGAGTACGCGTGTGTTAGG 180  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTGGC 1271  
QY 121 CTGCTCCGATGTACGGGCCAGATATTCGCGTATCTGAGGAGTACGCGTGTGTTAGG 180  
Db 1272 CTGCTCCGATGTACGGGCCAGATATTCGCGTATCTGAGGAGTACGCGTGTGTTAGG 1331  
QY 181 CGAAAGCGGGGCTTCGCTTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 1332 CGCCACGCGGGCTTCGCTTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 1391  
QY 241 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
Db 1392 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 1451  
QY 301 TAAAGTAAAGTGTAGCAACATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 360  
Db 1452 TAAAGTAAAGTGTAGCAACATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 1511  
QY 361 TGGAAAGTAAAGTGTAGCAACATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 420  
Db 1512 TGGAAAGTAAAGTGTAGCAACATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 1571  
QY 421 TTGAGCAACCACTAAATTCGGATTGCGATGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1572 TTGAGCAACCACTAAATTCGGATTGCGATGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631  
QY 480 ACAATAAGCCCATTTGACCAATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCCCATTTGACCAATTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 44  
AR302366  
LOCUS AR302366 9737 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 28 from patent US 6541221.  
ACCESSION AR302366  
VERSION AR302366.1 GI:31690620  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9737)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 28 01-APR-2003;  
FEATURES Location/Qualifiers  
source 1..9737  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 1211  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTGGC 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAATCTGTAGGTTAGGCGTTTGGC 1271  
QY 121 CTGCTCCGATGTACGGGCCAGATATTCGCGTATCTGAGGAGTACGCGTGTGTTAGG 180  
Db 1272 CTGCTCCGATGTACGGGCCAGATATTCGCGTATCTGAGGAGTACGCGTGTGTTAGG 1331  
QY 181 CGAAAGCGGGGCTTCGCTTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 1332 CGCCACGCGGGCTTCGCTTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 1391  
QY 241 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
Db 1392 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 1451  
QY 301 TAAAGTAAAGTGTAGCAACATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 360  
Db 1452 TAAAGTAAAGTGTAGCAACATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 1511  
QY 361 TGGAAAGTAAAGTGTAGCAACATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 420  
Db 1512 TGGAAAGTAAAGTGTAGCAACATCGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 1571  
QY 421 TTGAGCAACCACTAAATTCGGATTGCGATGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
Db 1572 TTGAGCAACCACTAAATTCGGATTGCGATGCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631  
QY 480 ACAATAAGCCCATTTGACCAATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1632 ACAATAAGCCCATTTGACCAATTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 45  
AR373232  
LOCUS AR373232 9737 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 22 from patent US 6602686.  
ACCESSION AR373232  
VERSION AR373232.1 GI:40075240  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

```

Unclassified.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 22 05-AUG-2003;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 95.8%; Score 500.8; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-141;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTAGTGTGCGGCGGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGTGGAGTTCGCTAGTGTGCGGCGGCAAAATTTAAGCTACA 1211

QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 120
DB 1212 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 1271

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180
DB 1272 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 1331

QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 240
DB 1332 CGCCAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 1391

QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 300
DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 1451

QY 301 TAAGATGATGTAGCAACATGCCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGG 360
DB 1452 TAAGATGATGTAGCAACATGCCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGG 1511

QY 361 TGGAGTATAGGTGTGATGATGCGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420
DB 1512 TGGAGTATAGGTGTGATGATGCGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 1571

QY 421 TTGGACGACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479
DB 1572 TTGGACGACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631

QY 480 ACAATAAGCCATTGACCAATTCACCATTTGGTGTGCACCTC 523
DB 1632 ACAATAAGCCATTGACCAATTCACCATTTGGTGTGCACCTC 1675

RESULT 46
AR373233
LOCUS AR373233 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6602686.
ACCESSION AR373233
VERSION AR373233.1 GI:40075241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 22 05-AUG-2003;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 95.8%; Score 500.8; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-141;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTAGTGTGCGGCGGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGTGGAGTTCGCTAGTGTGCGGCGGCAAAATTTAAGCTACA 1211

QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 120
DB 1212 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 1271

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180
DB 1272 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 1331

QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 240
DB 1332 CGCCAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 1391

QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 300
DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 1451

QY 301 TAAGATGATGTAGCAACATGCCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGG 360
DB 1452 TAAGATGATGTAGCAACATGCCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGG 1511

QY 361 TGGAGTATAGGTGTGATGATGCGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420
DB 1512 TGGAGTATAGGTGTGATGATGCGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 1571

QY 421 TTGGACGACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479
DB 1572 TTGGACGACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631

QY 480 ACAATAAGCCATTGACCAATTCACCATTTGGTGTGCACCTC 523
DB 1632 ACAATAAGCCATTGACCAATTCACCATTTGGTGTGCACCTC 1675

RESULT 46
AR373233
LOCUS AR373233 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6602686.
ACCESSION AR373233
VERSION AR373233.1 GI:40075241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 23 05-AUG-2003;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

```

```

Query Match 95.8%; Score 500.8; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-141;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTAGTGTGCGGCGGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGTGGAGTTCGCTAGTGTGCGGCGGCAAAATTTAAGCTACA 1211

QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 120
DB 1212 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 1271

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180
DB 1272 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 1331

QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 240
DB 1332 CGCCAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 1391

QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 300
DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGG 1451

QY 301 TAAGATGATGTAGCAACATGCCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGG 360
DB 1452 TAAGATGATGTAGCAACATGCCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGG 1511

QY 361 TGGAGTATAGGTGTGATGATGCGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420
DB 1512 TGGAGTATAGGTGTGATGATGCGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 1571

QY 421 TTGGACGACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479
DB 1572 TTGGACGACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631

QY 480 ACAATAAGCCATTGACCAATTCACCATTTGGTGTGCACCTC 523
DB 1632 ACAATAAGCCATTGACCAATTCACCATTTGGTGTGCACCTC 1675

RESULT 47
AR373238
LOCUS AR373238 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 28 from patent US 6602686.
ACCESSION AR373238
VERSION AR373238.1 GI:40075246
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 28 05-AUG-2003;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 95.8%; Score 500.8; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-141;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTAGTGTGCGGCGGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGTGGAGTTCGCTAGTGTGCGGCGGCAAAATTTAAGCTACA 1211

QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGC 120

```

Db	1392	TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCAACATGG	1451
Qy	301	TAACGATGAGTTAGCAACAATGCTTTACAAAGGAGAGAAAAGCACCGTGCAATGCCGATGG	360
Db	1452	TAACGATGAGTTAGCAACAATGCTTTACAAAGGAGAGAAAAGCACCGTGCAATGCCGATGG	1511
Qy	361	TGGAAGTAGAGTGTACGATCGTCCTTATTAAGAGGCAACAGACGGGTCTGACATGGA	420
Db	1512	TGGAAGTAGAGTGTACGATCGTCCTTATTAAGAGGCAACAGACGGGTCTGACATGGA	1571
Qy	421	TTTGGACGACCACTAAATTCGCATTCGACAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT	479
Db	1572	TTTGGACGACCACTAAATTCGCATTCGACAGAT-ATTGTATTTAAAGTGCCTAGCTCGAT	1631
Qy	480	ACAATAAACGCCATTGTACCAATTCACCAATTCGTTGCAACCTC	523
Db	1632	ACAATAAACGCCATTGTACCAATTCACCAATTCGTTGCAACCTC	1675
RESULT 49			
AR401619			
LOCUS	AR401619	9737 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 23 from patent US 6623958.		
ACCESSION	AR401619		
VERSION	AR401619.1	GI:40149067	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 9737)		
AUTHORS	Harrington,J.J., Sherf,B. and Rundlett,S.		
TITLE	Compositions and methods for non-targeted activation of endogenous genes		
JOURNAL	Patent: US 6623958-A 23 23-SEP-2003;		
FEATURES	Location/Qualifiers		
source	1..9737		
	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match	95.8%;	Score 500.8;	DB 6; Length 9737;
Best Local Similarity	98.5%;	Pred. No. 1.9e-141;	
Matches 516;	Conservative 0;	Mismatches 7;	Indels 1; Gaps 1;
Qy	1	CTGCTCCCTGCTGTGTGTGTGTCGAGGTGCTGTAGTGTAGTCGCGAGCAAAATTTAAGCTACA	60
Db	1152	CTGCTCCCTGCTGTGTGTGTGTCGAGGTGCTGTAGTGTAGTCGCGAGCAAAATTTAAGCTACA	1211
Qy	61	ACAGCGCAAGGCTTGACCGCAACTGCATGAGAAATCTGCTTAGGTTAGGCGTTTTCGG	120
Db	1212	ACAGCGCAAGGCTTGACCGCAANTGCATGAGAAATCTGCTTAGGTTAGGCGTTTTCGG	1271
Qy	121	CTGCTTCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGCACTAGGGTGTGTTTAGG	180
Db	1272	CTGCTTCGCGATGTACGGGCCAGATATCTGAGGGGCACTAGGGTGTGTTTAGG	1331
Qy	181	CGAAAGCGGGGCTTCGTTTGTACGGGTGTAGAGTCCCTCTCAGGATATAGTATTTCGC	240
Db	1332	CGCCACAGCGGGGCTTCGTTTGTACGGGTGTAGAGTCCCTCTCAGGATATAGTATTTCGC	1391
Qy	241	TTTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGTCAACATGG	300
Db	1392	TTTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGTCAACATGG	1451
Qy	301	TAACGATGAGTTAGCAACAATGCTTTACAAAGGAGAGAAAAGCACCGTGCAATGCCGATGG	360
Db	1452	TAACGATGAGTTAGCAACAATGCTTTACAAAGGAGAGAAAAGCACCGTGCAATGCCGATGG	1511
Qy	361	TGGAAGTAGAGTGTACGATCGTCCTTATTAAGAGGCAACAGACGGGTCTGACATGGA	420
Db	1512	TGGAAGTAGAGTGTACGATCGTCCTTATTAAGAGGCAACAGACGGGTCTGACATGGA	1571







Db 1406 CTGCTTCGGGATGTACGGGCCAGATATACGGGTATCTGAGGGGACTAGGTGTGTTAGG 1465  
QY 181 CGAAAGCGGGGCTTCGGTTGTACCGGGTTAGAGTCCCTTCAGGATATAGTAGTTTCGC 240  
Db 1466 CGCCAGCGGGGCTTCGGTTGTACCGGGTTAGAGTCCCTTCAGGATATAGTAGTTTCGC 1525  
QY 241 TTTTTCATAGGGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTGCACATGG 300  
Db 1526 TTTTTCATAGGGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTGCACATGG 1585  
QY 301 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGG 360  
Db 1586 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGG 1645  
QY 361 TGGAGTAAAGTGTAGTACGTCGCTTATAGGAGGCAACACCGGTCGACATGGA 420  
Db 1646 TGGAGTAAAGTGTAGTACGTCGCTTATAGGAGGCAACACCGGTCGACATGGA 1705  
QY 421 TTTGACGAAACACCTAAATTCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1706 TTTGACGAAACACCTAAATTCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1765  
QY 480 ACAATAAACGCCATTGACATTCACCAATTCGACATTCGTCGACCTC 523  
Db 1766 ACAATAAACGCCATTGACATTCACCAATTCGTCGACCTC 1809  
  
RESULT 55  
AR215121  
LOCUS AR215121 10060 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 25 from patent US 6410266.  
ACCESSION AR215121  
VERSION AR215121.1 GI:23313249  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10060)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6410266-A 25 25-JUN-2002;  
FEATURES  
source Location/Qualifiers  
1..10060  
/organism="unknown"  
/mol\_type="genomic DNA"  
  
ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 10060;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
  
QY 1 CTGCTCCCTGCTTGTGTGTGAGGTCCCTGAGTACTGCGGAGCAAAATTAAGCTACA 60  
Db 1475 CTGCTCCCTGCTTGTGTGTGAGGTCCCTGAGTACTGCGGAGCAAAATTAAGCTACA 1534  
QY 61 ACAAGGCAAGGCTTACCGCAATTCGATGAAGATCTCTTAGGGTTAGCGCTTTTGG 120  
Db 1535 ACAAGGCAAGGCTTACCGCAATTCGATGAAGATCTCTTAGGGTTAGCGCTTTTGG 1594  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 1595 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 1654  
QY 181 CGAAAGCGGGGCTTCGGTTGTACCGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 1655 CGCCAGCGGGGCTTCGGTTGTACCGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 1714  
QY 241 TTTTTCATAGGGAGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTGCACATGG 300  
Db 1715 TTTTTCATAGGGAGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTGCACATGG 1774  
QY 301 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGG 360  
Db 1715 TTTTTCATAGGGAGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTGCACATGG 1774  
QY 301 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGG 360

Db 1775 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGG 1834  
QY 361 TGGAGTAAAGTGTAGTACGTCGCTTATAGGAGGCAACACCGGTCGACATGGA 420  
Db 1835 TGGAGTAAAGTGTAGTACGTCGCTTATAGGAGGCAACACAGACAGTCTGACATGGA 1894  
QY 421 TTTGACGAAACACCTAAATTCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1895 TTTGACGAAACACCTAAATTCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1954  
QY 480 ACAATAAACGCCATTGACATTCACCAATTCGTCGTCGACCTC 523  
Db 1955 ACAATAAACGCCATTGACATTCACCAATTCGTCGTCGACCTC 1998  
  
RESULT 56  
AR302363  
LOCUS AR302363 10060 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 25 from patent US 6541221.  
ACCESSION AR302363  
VERSION AR302363.1 GI:31690617  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10060)  
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
TITLE Compositions and methods for non-targeted activation of endogenous genes  
JOURNAL Patent: US 6541221-A 25 01-APR-2003;  
FEATURES  
source Location/Qualifiers  
1..10060  
/organism="unknown"  
/mol\_type="genomic DNA"  
  
ORIGIN  
Query Match 95.8%; Score 500.8; DB 6; Length 10060;  
Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
  
QY 1 CTGCTCCCTGCTTGTGTGTGAGGTCCCTGAGTACTGCGGAGCAAAATTAAGCTACA 60  
Db 1475 CTGCTCCCTGCTTGTGTGTGAGGTCCCTGAGTACTGCGGAGCAAAATTAAGCTACA 1534  
QY 61 ACAAGGCAAGGCTTACCGCAATTCGATGAAGATCTCTTAGGGTTAGCGCTTTTGG 120  
Db 1535 ACAAGGCAAGGCTTACCGCAATTCGATGAAGATCTCTTAGGGTTAGCGCTTTTGG 1594  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 1595 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 1654  
QY 181 CGAAAGCGGGGCTTCGGTTGTACCGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 1655 CGCCAGCGGGGCTTCGGTTGTACCGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 1714  
QY 241 TTTTTCATAGGGAGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTGCACATGG 300  
Db 1715 TTTTTCATAGGGAGGGGGAATGTAGTCTTATGCAATATCTTTGTAGTCTTGCACATGG 1774  
QY 301 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGG 360  
Db 1775 TAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGG 1834  
QY 361 TGGAGTAAAGTGTAGTACGTCGCTTATAGGAGGCAACACAGACGGTCTGACATGGA 420  
Db 1835 TGGAGTAAAGTGTAGTACGTCGCTTATAGGAGGCAACACAGACGGTCTGACATGGA 1894  
QY 421 TTTGACGAAACACCTAAATTCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 1895 TTTGACGAAACACCTAAATTCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1954

QY 480 ACAATAAAGCGCAATTCACCATTCACCATTCAGTGTGACCTC 523  
 Db 1955 ACAATAAAGCGCAATTCACCATTCACCATTCAGTGTGACCTC 1998

RESULT 57  
 AR373235  
 LOCUS 10060 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 25 from patent US 6602686.  
 AR373235  
 ACCESSION  
 AR373235.1 GI:40075243  
 VERSION  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 10060)  
 AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
 TITLE Compositions and Method for non-targeted activation of endogenous genes  
 JOURNAL Patent: US 6602686-A 25 05-AUG-2003;  
 FEATURES Location/Qualifiers  
 source 1..10060  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 95.8%; Score 500.8; DB 6; Length 10060;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGCAGCAAAATTAAGTACA 60  
 Db 1475 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGCAGCAAAATTAAGTACA 1534

QY 61 ACAGGCAAGGCTTCACCGCAATTCGATGAAGAATCTGTTAGGTTAGCGTTTGG 120  
 Db 1535 ACAGGCAAGGCTTCACCGCAATTCGATGAAGAATCTGTTAGGTTAGCGTTTGG 1594

QY 121 CTGCTCCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGTTGTTAGG 180  
 Db 1595 CTGCTCCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGTTGTTAGG 1654

QY 181 CGAAGACGGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 240  
 Db 1655 CGCCACGGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 1714

QY 241 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATACCTTTGAGTCTTGCAACATGG 300  
 Db 1715 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATACCTTTGAGTCTTGCAACATGG 1774

QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
 Db 1775 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1834

QY 361 TGGAGTAAAGGTTGATCGATCGCTTATAGGAAGGCAACAGCGGTTCTGACATGA 420  
 Db 1835 TGGAGTAAAGGTTGATCGATCGCTTATAGGAAGGCAACAGCGGTTCTGACATGA 1894

QY 421 TTGAGCAACCACTAAATTCGGATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 Db 1895 TTGAGCAACCACTAAATTCGGATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1954

QY 480 ACAATAAGCCCAATTCACCATTCACCATTCAGTGTGACCTC 523  
 Db 1955 ACAATAAGCCCAATTCACCATTCACCATTCAGTGTGACCTC 1998

RESULT 58  
 AR401621  
 LOCUS 10060 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 25 from patent US 6623958.  
 AR401621  
 ACCESSION  
 AR401621.1 GI:40149069  
 VERSION

KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 10060)  
 AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.  
 TITLE Compositions and methods for non-targeted activation of endogenous genes  
 JOURNAL Patent: US 6623958-A 25 23-SEP-2003;  
 FEATURES Location/Qualifiers  
 source 1..10060  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 95.8%; Score 500.8; DB 6; Length 10060;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-141;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGCAGCAAAATTAAGTACA 60  
 Db 1475 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGCAGCAAAATTAAGTACA 1534

QY 61 ACAGGCAAGGCTTCACCGCAATTCGATGAAGAATCTGTTAGGTTAGCGTTTGG 120  
 Db 1535 ACAGGCAAGGCTTCACCGCAATTCGATGAAGAATCTGTTAGGTTAGCGTTTGG 1594

QY 121 CTGCTCCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGTTGTTAGG 180  
 Db 1595 CTGCTCCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGTTGTTAGG 1654

QY 181 CGAAGACGGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 240  
 Db 1655 CGCCACGGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTATTGCG 1714

QY 241 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATACCTTTGAGTCTTGCAACATGG 300  
 Db 1715 TTTTGCATAGGAGGGGGAATCTAGTCTTATGCAATACCTTTGAGTCTTGCAACATGG 1774

QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
 Db 1775 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1834

QY 361 TGGAGTAAAGGTTGATCGATCGCTTATAGGAAGGCAACAGCGGTTCTGACATGA 420  
 Db 1835 TGGAGTAAAGGTTGATCGATCGCTTATAGGAAGGCAACAGCGGTTCTGACATGA 1894

QY 421 TTGAGCAACCACTAAATTCGGATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 Db 1895 TTGAGCAACCACTAAATTCGGATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1954

QY 480 ACAATAAGCCCAATTCACCATTCACCATTCAGTGTGACCTC 523  
 Db 1955 ACAATAAGCCCAATTCACCATTCACCATTCAGTGTGACCTC 1998

RESULT 59  
 AX031159  
 LOCUS 11265 bp DNA circular PAT 20-SEP-2000  
 DEFINITION Sequence 1 from Patent WO9844129.  
 AX031159  
 ACCESSION  
 AX031159.1 GI:10278512  
 VERSION  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1  
 Lew,A.M., Boyle,J.S. and Brady,J.L.  
 AUTHORS Enhancement of immune response using targeting molecules  
 TITLE Patent: WO 9844129-A 1 08-OCT-1998;  
 JOURNAL INST MEDICAL W & E HALL (AU) ; QUEENSLAND INST MED RES (AU) ; CSL LTD (AU) ; LEW ANDREW MARK (AU) ; UNIV MELBOURNE (AU) ; BOYLE JEFFEREY STEPHEN (AU) ; BRADY JAMIE LOUISE (AU) ; COMW SCIENT IND

```

FEATURES
  source
    1..11265
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

ORIGIN
  Query Match 95.8%; Score 500.8; DB 6; Length 11265;
  Best Local Similarity 98.5%; Pred. No. 1.9e-141;
  Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 110 CTGCTCCCTGCTGTGTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 169
QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGGTTAGCGTTTGGG 120
DB 170 ACAAGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGGTTAGCGTTTGGG 229
QY 121 CTGCTCCCTGCTGTGTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 180
DB 230 CTGCTCCCTGCTGTGTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 289
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 240
DB 290 CGCCAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 349
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300
DB 350 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 409
QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 360
DB 410 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 469
QY 361 TGGAGTAAGTGGTGCATGCGCTTATTAGGAGCAACAGACGGTCTGACATGA 420
DB 470 TGGAGTAAGTGGTGCATGCGCTTATTAGGAGCAACAGACGGTCTGACATGA 529
QY 421 TTGGACGACCACTAAATTCGGATTCGAGAT-ATTGTATTAGTGGCTAGCTCGAT 479
DB 530 TTGGACGACCACTAAATTCGGATTCGAGAT-ATTGTATTAGTGGCTAGCTCGAT 589
QY 480 ACAATAAGCGCATTTGACCACTTCCACATTTGGTGTGCACCTC 523
DB 590 ACAATAAGCGCATTTGACCACTTCCACATTTGGTGTGCACCTC 633

RESULT 60
BD084805 11265 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Enhancement of immune response using targeting molecules.
ACCESSION BD084805
VERSION JP 2001522235-A/1.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 11265)
AUTHORS Boyle,J.S., Brady,J.L. and Lew,A.M.
TITLE Enhancement of immune response using targeting molecules
JOURNAL Patent: JP 2001522235-A 1 13-NOV-2001;
THE COUNCIL OF THE QUEENSLAND INSTITUTE OF MEDICAL RESEARCH,
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, THE
UNIVERSITY OF MELBOURNE, THE WALTER AND ELIZA HALL INSTITUTE OF
MEDICAL RESEARCH, CSL LTD
COMMENT OS Unidentified
PN JP 2001522235-A/1
PD 13-NOV-2001
PF 26-MAR-1998 AU PP 1998540989
PR 27-MAR-1997 AU PP05891.13-FEB-1998 AU PP 1830 PI
JEFFEREY STEPHEN BOYLE, JAMIE LOUISE BRADY, ANDREW MARK LEW PC

```

```

FEATURES
  source
    1..11265
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

ORIGIN
  Query Match 95.8%; Score 500.8; DB 6; Length 11265;
  Best Local Similarity 98.5%; Pred. No. 1.9e-141;
  Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 110 CTGCTCCCTGCTGTGTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 169
QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGGTTAGCGTTTGGG 120
DB 170 ACAAGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGGTTAGCGTTTGGG 229
QY 121 CTGCTCCCTGCTGTGTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 180
DB 230 CTGCTCCCTGCTGTGTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 289
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 240
DB 290 CGCCAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 349
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300
DB 350 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 409
QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 360
DB 410 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 469
QY 361 TGGAGTAAGTGGTGCATGCGCTTATTAGGAGCAACAGACGGTCTGACATGA 420
DB 470 TGGAGTAAGTGGTGCATGCGCTTATTAGGAGCAACAGACGGTCTGACATGA 529
QY 421 TTGGACGACCACTAAATTCGGATTCGAGAT-ATTGTATTAGTGGCTAGCTCGAT 479
DB 530 TTGGACGACCACTAAATTCGGATTCGAGAT-ATTGTATTAGTGGCTAGCTCGAT 589
QY 480 ACAATAAGCGCATTTGACCACTTCCACATTTGGTGTGCACCTC 523
DB 590 ACAATAAGCGCATTTGACCACTTCCACATTTGGTGTGCACCTC 633

RESULT 61
AR202606 565 bp DNA linear PAT 20-JUN-2002
LOCUS
DEFINITION Sequence 13 from patent US 6365151.
ACCESSION AR202606
VERSION AR202606.1 GI:21498779
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 565)
AUTHORS Halpern,M.S. and England,J.M.
TITLE Cellular immunogens comprising cognate proto-oncogenes
JOURNAL Patent: US 6365151-A 13 02-APR-2002;
FEATURES Location/Qualifiers
  source
    1..565
    /organism="unknown"
    /mol_type="unassigned DNA"

```

C12N15/62, C07K19/00, A61K39/00, A61K48/00

CC Strandedness: Double;  
 CC Topology: Circular;  
 CC Enhancement of immune response using targeting molecules FH  
 Key Location/Qualifiers  
 FT source 1..11265  
 /organism='Unidentified'.

ORIGIN

Query Match 90.2%; Score 472; DB 6; Length 565;  
 Best Local Similarity 98.0%; Pred. No. 1.2e-132;  
 Matches 490; Conservative 0; Mismatches 5; Indels 5; Gaps 1;

QY 28 GCTGAGTAGTGGCGGAGCAAAATTTAAGCTACAAAGGCAAGGCTTGACCGCAAAATTCG 87  
 DB 1 GCTGAGTAGTGGCGGAGCAAAATTTAAGCTACAAAGGCAAGGCTTGACCGCAAAATTCG 60

QY 88 ATGAAGAAATCTCTTTAGGGTTAGGCGTTTTCGGTCTCGCATGATGATACGGGCGAGATAT 147  
 DB 61 ATGAAGAAATCTCTTTAGGGTTAGGCGTTTTCGGTCTCGCATGATGATACGGGCGAGATAT 120

QY 148 TCGCGTATCTGAGGGGACTAGGCTGTGTTAGGCGAAAGCGGGGCTTCGTTGTACGGG 207  
 DB 121 ACGCGTATCTGAGGGGACTAGGCTGTGTTAGGCGAAAGCGGGGCTTCGTTGTACGGG 180

QY 208 GTTAGGAGTCCCTCCAGGATATAGTAGTTTCGCTTTTTCATAGGAGGGGGAATGTAGT 267  
 DB 181 GTTAGGAGTCCCTCCAGGATATAGTAGTTTCGCTTTTTCATAGGAGGGGAATGTAGT 240

QY 268 CTTATGCAATATCTTTGTAGTCTTGCACATG-----GTAAAGATGATAGCAATGC 322  
 DB 241 CTTATGCAATATCTTTGTAGTCTTGCACATGCTTATGTAACGATGAGTTAGCAATGC 300

QY 323 CTTACAGGAGAGAAAGCAACCGTCGATGCCGATTGTTGGAAGTAAGTGTGTACGATCG 382  
 DB 301 CTTACAGGAGAGAAAGCAACCGTCGATGCCGATTGTTGGAAGTAAGTGTGTACGATCG 360

QY 383 TGCCTTATTAGGAGCAACAGACGGGCTCTGACATGATGATGAGCAACCACTAAATTCG 442  
 DB 361 TGCCTTATTAGGAGCAACAGACGGGCTCTGACATGATGATGAGCAACCACTAAATTCG 420

QY 443 CATTCGAGAGATTTGTTTATTTAGTCTGCTAGCTGATGATGATGATGATGATGATGAT 502  
 DB 421 CATTCGAGAGATTTGTTTATTTAGTCTGCTAGCTGATGATGATGATGATGATGATGAT 480

QY 503 CACCACATTTGGTGCACCT 522  
 DB 481 CACCACATTTGGTGCACCT 500

RESULT 62  
 LOCUS BD005483 565 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Cellular immunogens useful cancer vaccines.  
 ACCESSION BD005483  
 VERSION BD005483.1 GI:18633854  
 KEYWORDS JP 2001501909-A/13.  
 SOURCE unclassified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 565)  
 AUTHORS Halpern,M.S. and England,J.M.  
 TITLE Cellular immunogens useful cancer vaccines  
 JOURNAL Patent: JP 2001501909-A 13 13-FEB-2001;  
 ALLEGHENY UNIVERSITY OF THE HEALTH SCIENCES  
 COMMENT OS Unidentified  
 PN JP 2001501909-A/13  
 PD 13-FEB-2001  
 PF 13-JAN-1997 JP 1997526124  
 PR 19-JAN-1996 US 60/010262  
 PI MICHAEL S HALPERN,JAMES M ENGLAND  
 PC A01K63/00,A61K39/00,A61K39/38,A61K48/00,C12N5/00,C12N15/00 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1..565  
 FT /organism='Unidentified'.  
 FT Location/Qualifiers  
 1..565  
 /organism='unidentified'

ORIGIN

Query Match 90.2%; Score 472; DB 6; Length 565;  
 Best Local Similarity 98.0%; Pred. No. 1.2e-132;  
 Matches 490; Conservative 0; Mismatches 5; Indels 5; Gaps 1;

QY 28 GCTGAGTAGTGGCGGAGCAAAATTTAAGCTACAAAGGCAAGGCTTGACCGCAAAATTCG 87  
 DB 1 GCTGAGTAGTGGCGGAGCAAAATTTAAGCTACAAAGGCAAGGCTTGACCGCAAAATTCG 60

QY 88 ATGAAGAAATCTCTTTAGGGTTAGGCGTTTTCGGTCTTCGATGATGATACGGGCGAGATAT 147  
 DB 61 ATGAAGAAATCTCTTTAGGGTTAGGCGTTTTCGGTCTTCGATGATGATACGGGCGAGATAT 120

QY 148 TCGCGTATCTGAGGGGACTAGGCTGTGTTAGGCGAAAGCGGGGCTTCGTTGTACGGG 207  
 DB 121 ACGCGTATCTGAGGGGACTAGGCTGTGTTAGGCGAAAGCGGGGCTTCGTTGTACGGG 180

QY 208 GTTAGGAGTCCCTCCAGGATATAGTAGTTTCGCTTTTTCATAGGAGGGGGAATGTAGT 267  
 DB 181 GTTAGGAGTCCCTCCAGGATATAGTAGTTTCGCTTTTTCATAGGAGGGGAATGTAGT 240

QY 268 CTTATGCAATATCTTTGTAGTCTTGCACATG-----GTAAAGATGATAGCAATGC 322  
 DB 241 CTTATGCAATATCTTTGTAGTCTTGCACATGCTTATGTAACGATGAGTTAGCAATGC 300

QY 323 CTTACAGGAGAGAAAGCAACCGTCGATGCCGATTGTTGGAAGTAAGTGTGTACGATCG 382  
 DB 301 CTTACAGGAGAGAAAGCAACCGTCGATGCCGATTGTTGGAAGTAAGTGTGTACGATCG 360

QY 383 TGCCTTATTAGGAGCAACAGACGGGCTCTGACATGATGATGAGCAACCACTAAATTCG 442  
 DB 361 TGCCTTATTAGGAGCAACAGACGGGCTCTGACATGATGATGAGCAACCACTAAATTCG 420

QY 443 CATTCGAGAGATTTGTTTATTTAGTCTGCTAGCTGATGATGATGATGATGATGATGAT 502  
 DB 421 CATTCGAGAGATTTGTTTATTTAGTCTGCTAGCTGATGATGATGATGATGATGATGAT 480

QY 503 CACCACATTTGGTGCACCT 522  
 DB 481 CACCACATTTGGTGCACCT 500

RESULT 63  
 LOCUS U41728 565 bp DNA linear VRL 19-JUL-2001  
 DEFINITION Rous sarcoma virus Schmidt-Ruppin subgroup A (NY) clone SRA-V,  
 v-src gene, partial cds, and 3'LTR.  
 ACCESSION U41728  
 VERSION U41728.1 GI:1136591  
 KEYWORDS Rous sarcoma virus  
 ORGANISM Rous sarcoma virus  
 REFERENCE 1 (bases 1 to 565)  
 AUTHORS Hara,H. and Kaj,A.  
 TITLE The U3 region of the long terminal repeat of a subgroup A transformation-defective rous sarcoma virus (tdPHE2010) converts a noncytopathic virus to a cytopathic virus  
 Virus Genes 15 (2), 171-180 (1997)  
 JOURNAL 98083689  
 MEDLINE 9421881  
 PUBMED 9421881  
 REFERENCE 2 (bases 1 to 565)  
 AUTHORS Hara,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-DEC-1995) Hiroto Hara, University of Pennsylvania School of Medicine, Microbiology, 573 Maloney Building, 36th and Spruce Street, Philadelphia, PA 19104-4283, USA  
 3 (sites)  
 REFERENCE Takeya,T., Hanafusa,H., Jurchans,R.P., Ju,G. and Skalka,A.M.  
 AUTHORS Comparison between the viral transforming gene (src) of recovered

D<sub>b</sub> 361 TGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCAACCGAATTCG 420

```
mat_peptide 909.1082
```

3  
3  
4  
. .  
>  
>  
3  
3  
3  
3  
3  
3  
3  
3  
3  
3  
3

/gene="gag"  
product="reading frame p10"  
1083..1802  
/gene="gag"  
product="reading frame p27"  
1830..2096  
/gene="gag"  
product="reading frame p12"  
2097..2468  
/gene="gag"  
product="reading frame p15"  
2489..5173  
/gene="pol"  
2489..5173  
/gene="pol"  
product="reverse transcriptase"  
/note="stop codon taa follows at 5174-5176."  
5064..6884  
/gene="env"  
5064..6884  
/gene="env"  
product="envelope protein"  
/note="stop codon taa follows at 6885-6887."  
7267..8847  
/gene="src"  
7267..8847  
/gene="src"  
/note="transforming gene"  
/codon\_start=1  
product="tyrosine kinase"  
/protein\_id="BA01500.1"  
/db\_xref="GI:1221014"  
/translation="MGSSKSFDPQSRSLEPPDSTHHGGFPASQTNNTAAAPDTH  
RPPRSFGTVAEPKLPFGDFNTSITVSPORAGALAGGVTTFVALVDYESWTEDLGF  
KGERLOIVNNTGNWLAHSVTTGOTYIPSNVAPSDSQAEWVFGKJTRRESER  
LLLPQPRCTFSRSESTTKAYCLSVDFPNKAGLNKHVKRLKLDGGFYTSRT  
QSSLLQVITTKSHADGLCHRLINVCPTQGLAKDWEIPRESURLEVLGGG  
CFGEVWGTVNGTFRVATKLPKTPSPFAFQEAQVMKLOHEKLVQIYAVVEEPI  
YVIEYKSGSLNLFKGMGKYLRLPOLVDMAAQIASSMAVYVRMYVVRDLRAANI  
LVGENLVKVDGFLARLIEDNEVYTAQGAQKPIKWTAPEAALYGRFTIKSDVWSFGI  
LLETUWKGVVPYGMGNGEVLDRVESGYMPCPECPESLHDLMCQWRDPBERT  
FRYLAQLLPACVLEAE"  
9071..9296  
/note="U3 region"  
9297..9317  
/note="R region"  
  
ORIGIN  
Query Match 90.0%; Score 470.5; DB 14; Length 9317;  
Best local similarity 96.7%; Pred. No. 3.2e-132;  
Matches 492; Conservative 0; Mismatches 14; Indels 3; Gaps 1;  
  
QY 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCGGCGAGCAAAATTAAAGCTACA 60  
DB 8812 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGCGGCGAGCAAAATTAAAGCTACA 8871  
  
QY 61 ACAAGCAAGGCTGACCGACAAATTCATGAAGAATCTGCTAGCGGTAGCGGTTTTCGG 120  
DB 8872 ACAAGCAAGGCTGCGCGACAAATTCATGAAGAATCTGCTAGCGGTAGCGGTTTTCGG 8931  
  
QY 121 CTGCTTCGATGTACGGCGCAGATTTCCGCTATCTGAGGGGACCTAGGCTGTCTTAGG 180  
DB 8932 CTGCTTCGATGTACGGCGCAGATTTCCGCTATCTGAGGGGACCTAGGCTGTCTTAGG 8991  
  
QY 181 CGAAAACGGGGCTTCGGTGTACCGGTTAGGAGTCCCTCCTCAGGATATAGTAGTTTCGC 240  
DB 8992 CGAAAACGGGGCTTCGGTGTACCGGTTAGGAGTCCCTCCTCAGGATATAGTAGTTTCGC 9051  
  
QY 241 TTTTGCATAGGAGGGGAAATGTAGCTTTATGCAATACCTCTGTAGTCTTTCGCAACATGG 300  
DB 9052 TTTTGCATAGGAGGGGAAATGTAGCTTTATGCAATACCTCTGTAGTCTTTCGCAACATGG 9108  
  
QY 301 TAACGATAGTAGTACACATGCCCTTACAGGAGAGAAAGCACCCTGCATGCCGATTGG 360

Db 9109 TAAAGATGAGTTAGCAACATGCTTACAGAGGAGGAAAGACACCGCTGCATGACGATTGG 9168  
QY 361 TGGAGTTRAGGTGGTACGATGTCGCTTATTAGGAGGACCAAGACGGGTCTGACATGGA 420  
Db 9169 TGGAGTTRAGGTGGTACGATGTCGCTTATTAGGAGGACCAAGACGGGTCTGACATGGA 9228  
QY 421 TTGACGACCAACCACTAAATTCGGCATTTGCAGAGATATTGATTTTAAGTCCTAGCTCGATA 480  
Db 9229 TTGACGACCAACCACTAAATTCGGCATTTGCAGAGATATTGATTTTAAGTCCTAGCTCGATA 9288  
QY 481 CAATAAAGCCATTTGACCAATTCACCA 509  
Db 9289 CAATAAAGCCATTTGACCAATTCACCA 9317  
  
RESULT 65  
CVU64449 5647 bp DNA circular SYN 01-DEC-2000  
LOCUS Cloning vector pOPRSVIMCS from Lacswitch II System, complete  
DEFINITION  
ACCESSION U64449  
VERSION U64449.2 GI:4726082  
KEYWORDS  
SOURCE Cloning vector pOPRSVIMCS  
ORGANISM Cloning vector pOPRSVIMCS  
REFERENCE 1 (bases 1 to 5647)  
AUTHORS Wyborski, D.L.  
DIRECT SUBMISSION  
JOURNAL Submitted (18-JUL-1996) Genetic Systems, Stratagene, 11011 North  
Torrey Pines Road, La Jolla, CA 92037, USA  
REFERENCE 2 (bases 1 to 5647)  
AUTHORS Wyborski, D.L.  
DIRECT SUBMISSION  
JOURNAL Submitted (21-NOV-1997) Genetic Systems, Stratagene, 11011 North  
Torrey Pines Road, La Jolla, CA 92037, USA  
REMARK Sequence update by submitter  
REFERENCE 3 (bases 1 to 5647)  
AUTHORS Wyborski, D.L.  
DIRECT SUBMISSION  
JOURNAL Submitted (30-APR-1999) Genetic Systems, Stratagene, 11011 North  
Torrey Pines Road, La Jolla, CA 92037, USA  
REMARK Sequence update by submitter  
COMMENT On Apr 30, 1999 this sequence version replaced gi:3025466.  
FEATURES  
1..5647  
/organism="Cloning vector pOPRSVIMCS"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:50945"  
complement (241..1044)  
/codon\_start=1  
/transl\_table=11  
/product="neomycin resistance protein"  
/protein\_id="AAC12959.1"  
/db\_xref="GI:1515457"  
/translation="MGSAIEQQLHAGSPAAWVERLFGYDWAQTTIGCSDAAPFLSA  
QGRPLVFKYDLQSGALNELQDEAARLSWLATGVCFAAVLDVVTAGRWMLLGEVPG  
QLLSHLPAAKVSIMADAMERLHTLPATCPFDHAKHRIERARTMEAGLVQDD  
LDEEQLGAPAEIPLKAEKMPDGEDLVVTHGDACLPMIVENGRESGFTDCGRLGVA  
DRYQIALATRDIAELGEWADRFVLYGIAAPDSQRIAFYRLLEFF"  
complement (4587..5447)  
/codon\_start=1  
/transl\_table=11  
/product="beta-lactamase"  
/protein\_id="AAC12960.1"  
/db\_xref="GI:1515458"  
/translation="MSIQHFVALIPFAAFCLPVFAHPETLVKVKDAEDQLGARVGY  
IELDLNGSKLEDSFRPEEFPMSTFKVLLCGAVLSRIDAGCEQLGRIRHYQNQLVE  
YSPVTEKLTGMDTWRLESCAAITMSDNTAANLLITGGPKELTAPLHNMGDHYRL  
DWPEELNEAIPINDERDITMPVAMATTRLKLTGLLTLASRQLIDMWAEKAVGL  
LPSALPAGWFIADKSGAGERSGRIIAALPGDKPSRIIVYITGSGATMDERNQIA  
EIGASLIKHW"

## ORIGIN

Query Match 89.6%; Score 468.8; DB 12; Length 5647;  
Best Local Similarity 99.6%; Pred. No. 1.1e-131;  
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTTACA 60  
Db 2106 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTTACA 2165

Qy 61 ACAGGCAAGGCTTCACCGCAATTCGATGAAGATCTGTAGGTTAGCGTTTGGG 120  
Db 2166 ACAGGCAAGGCTTCACCGCAATTCGATGAAGATCTGTAGGTTAGCGTTTGGG 2225

Qy 121 CTGCTTCGGGATGACGGGCCAGATATTCGCGTATCTGAGGGACTAGGGTGTCTTACG 180  
Db 2226 CTGCTTCGGGATGACGGGCCAGATATTCGCGTATCTGAGGGACTAGGGTGTCTTACG 2285

Qy 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 2286 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 2345

Qy 241 TTTTGCATAGGAGGGGGAATAGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 2346 TTTTGCATAGGAGGGGGAATAGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 2405

Qy 301 TAAAGATAGGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
Db 2406 TAAAGATAGGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 2465

Qy 361 TGGAGTAAAGTGTACGATCGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
Db 2466 TGGAGTAAAGTGTACGATCGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 2525

Qy 421 TTGGACCAACCACTAAATTTCCGCAATTGCAGAGATATTCTATTAAAGTGCTTA 472  
Db 2526 TTGGACCAACCACTAAATTTCCGCAATTGCAGAGATATTCTATTAAAGTGCTTA 2577

## RESULT 66

XXU42372  
LOCUS Cloning vector pOPRSVicat 6243 bp DNA circular SYN 07-MAR-2000  
DEFINITION Cloning vector pOPRSVicat target vector from Lacswitch.  
ACCESSION U42372  
VERSION U42372.1 GI:1147761  
KEYWORDS Cloning vector pOPRSVicat  
SOURCE Cloning vector pOPRSVicat  
ORGANISM artificial sequences; vectors.  
REFERENCE 1 (bases 1 to 6243)  
AUTHORS Marsh, S.  
TITLE Direct Submission  
JOURNAL Submitted (05-DEC-1995) Sam Marsh, Marketing, Stratagene, 11011  
North Torrey Pines Road, La Jolla, CA 92037, USA  
FEATURES  
source  
1..6243  
/organism="Cloning vector pOPRSVicat"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:44739"

## ORIGIN

Query Match 89.6%; Score 468.8; DB 12; Length 6243;  
Best Local Similarity 99.6%; Pred. No. 1.1e-131;  
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTTACA 60  
Db 2106 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTAAGCTTACA 2165

Qy 61 ACAGGCAAGGCTTCACCGCAATTCGATGAAGATCTGTAGGTTAGCGTTTGGG 120  
Db 2166 ACAGGCAAGGCTTCACCGCAATTCGATGAAGATCTGTAGGTTAGCGTTTGGG 2225

Qy 121 CTGCTTCGGATGTACGGGCCAGATATTTCGCTATCTGAGGGACTAGGTTGTATTAGG 180  
Db 2226 CTGCTTCGGATGTACGGGCCAGATATTTCGCTATCTGAGGGACTAGGTTGTATTAGG 2285

Qy 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 2286 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 2345

Qy 241 TTTTGCATAGGAGGGGGAATAGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 2346 TTTTGCATAGGAGGGGGAATAGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 2405

Qy 301 TAAAGATAGGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
Db 2406 TAAAGATAGGTTAGCAACATGCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 2465

Qy 361 TGGAGTAAAGTGTACGATCGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
Db 2466 TGGAGTAAAGTGTACGATCGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 2525

Qy 421 TTGGACCAACCACTAAATTTCCGCAATTGCAGAGATATTCTATTAAAGTGCTTA 472  
Db 2526 TTGGACCAACCACTAAATTTCCGCAATTGCAGAGATATTCTATTAAAGTGCTTA 2577

RESULT 67  
AF052428  
LOCUS Rous sarcoma virus strain Schmidt-Ruppin B, complete genome. 9396 bp DNA linear VRL 01-APR-1998  
DEFINITION Rous sarcoma virus strain Schmidt-Ruppin B, complete genome.  
ACCESSION AF052428  
VERSION AF052428.1 GI:3003000  
KEYWORDS Rous sarcoma virus  
SOURCE Rous sarcoma virus  
ORGANISM Rous sarcoma virus  
REFERENCE 1 (bases 1 to 9396)  
AUTHORS Bouck, J., Skalka, A.M. and Katz, R.A.  
TITLE Complete nucleotide sequence of avian sarcoma virus  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 9396)  
AUTHORS Bouck, J., Skalka, A.M. and Katz, R.A.  
TITLE Direct Submission  
JOURNAL Submitted (04-MAR-1998) Fox Chase Cancer Center, 7701 Burholme Ave., Philadelphia, PA 19111, USA  
FEATURES  
source  
1..9396  
/organism="Rous sarcoma virus"  
/mol\_type="genomic DNA"  
/strain="Schmidt-Ruppin B"  
/db\_xref="taxon:11886"  
/clone="pLb6"  
LTR <1..101  
repeat\_region <1..21  
repeat\_region 22..101  
gene 399..6921  
CDS join(399..416,5097..6920)  
/codon\_start=1  
/product="envelope glycopolyprotein"  
/protein\_id="AAC08989.1"  
/db\_xref="GI:3003003"  
/translation="MEAVIKAVLTGYPGTSKSKKKPATSKKDKPEKTPLLPPTRVN  
YILIGLVLCVTVGVRAVHLLQPNGLMTWASPTGOTDFCLSTQASPTQCL  
GLPSPISGQDFKGVNDCTTLEPRLVSRGIGGPNSTLTLYQKVSCLLLKLVSL  
LDPELQGLQSLNLTNITRIPSVAGGCGTPTDPSFAGVVGWDRBRVTHILLTD  
PGNPPFPKSNSTGTGTWQSKFNFTPFSTVNCSTGSLNLSVSCCGCEPITLP  
PRAWVDSQGSFTKPKALPAFLICDRAWQGIKPSRPGVGPVYGLKLTMLAPNHFDI  
LKLANSRTGIRKRSVSHLDDTCSDEVQLWGPFTARIETASILAPGVAAQAALKEIR  
LACWSYKQNNITSLGLDDVTSIRHVLQNRALIDFLLIAGHGCGEDVAGNCCFN

```

LSHSBSIQKXQFMKEHVNKIGVDSDDPIGSMIRGLFGGIGEMAWHLLKGLLLGLVVI
LLAVVCLPCLLIQVCGNRXRMNNISYHYEYKLIKQAYQBPESRIV"
5265..6308
/gene="env"
/product="gp85"
6309..6617
/gene="env"
/product="gp37"
6618..7205
/gene="gag"
6619..7205
/gene="gag"
7206..7206
/codon_start=1
/product="structural polyprotein"
/protein_id="AAC08987.1"
/db_xref="GI:3003001"
/translocation="MEAVIKVVISSACKTVCGKTSKKEIGAMLISLLQKGLIMSPSD
LYSPGWDPIITAAISORAMVIGKSGELKTWGLVIGALKAAREEQVTSQAKFWLIGSD
GRVPPGPECIEKATERRIDKEGEVETTVQORDAKAPETATPKTVGTCYHCGTA
IGCNCAVASAPPVPGVGLYPSLGGQGGQGGTGRGAEQPRAEPOHAGLAPGPA
LTDNARIRELASTGPPVVPVAMPVVIKTEGPMTPEPKLITRLADTVRTKGLRSPITM
LEVALMSSPLPHDVTLMSEVILGPAPALMDANGVQLQTVIAAATDRHHPANQ
GRGERTNLRKGLADGAVNPGQQAALLRPGELVAITASALQAPREVARLAPAGPW
ADITQGSSEFVDFNRILKAVGSDSDPPSAPVLIIDCFQKSPDQQLIRAPST
LITTEGELIKVLDKRIAPLTDQGIAMASSAIQELVAVVNRERDQGTGGGARBL
CYTCGSPGHYQACPKRKSGNSRERCOLQDGMGNHAKQCRNRDSNQGQRFGLSSG
PWPYSEOPAVSLAMTMEKHDRPLVRVILNTGSHVQKORSVITALLDSGADITIEE
EDWPDVVDVDPANPOLHIGGGIPKXKSRDMLGVLNRDGSLSERPLLIPFVAVMYR
GSILGRSCLQGLGLRLTNL"
399..923
/gene="gag"
/product="p19"
930..1115
/gene="gag"
/product="p10"
1116..1835
/gene="gag"
/product="p27"
1836..2129
/gene="gag"
/product="p12"
2130..2501
/gene="gag"
/product="p15"
2522..5210
/gene="pol"
2522..5209
/gene="pol"
/codon_start=1
/product="polymerase and integrase protein"
/protein_id="AAC08988.1"
/db_xref="GI:3003002"
/translocation="TVALHAIPLKWKPDHTPVWIDOMPEGLKVALTOLVEKELQ
GHIESRSCANTPVFVIRXASGVYLLHDLRAVNAKLVPGAVQAGPVLSPALRGPW
LWVLDDKDFSIPLAEQDRFAFTLPSVNNQAAPARFQKVL PQMTCSTPICQLV
VQGVQLYGLKSLTYVAVGVLAEPRIATLNDVQKLVGSLQWLRLPALGIPRLMGPF
RYPQVGLSPNAREWLMKMAWREIVQLSTTAALRDWDPALPLEGAVRCEQGAIGV
LQGLSLTHPRPLLTFTOPTKAFMTAMLEVLITLILKLSASAVRTDGHVDFVLLIPAC
FREDIPLPEGLLALSGFAGKIRSDTPI:FDIARPLHSLKVRVTDHPVPQPTVTD
ASSSTHKVVWREGPRWEIKIADLGASVQQLERAVAMALLMPTTETNVVTDSPF
VAKMLLKQGVPESTAAAFILEDALQSRMAAVALHVRSHSEVFGFTFGNDVADSQ
ATFOYPLREAKDLHTLHIGRALSKACINSQOAREVQVTCPCNSAPALEAGVNP
RGILPQI:WQDFTLPRMAPRSMLAVTDVTASSAIVTVQGRVTSVAQPHWALIA
VLGRPKALKTNGSCFTSKTRELARWIAHTTIPGNSQOQAMVERANRLIKDIR
VLAEQDGMFKIIPASQOGLLAKAMVALNHPERGENTKTPQKHWRTVLITGPPVKI
RLTGEWKGWNLVWNGRTAAVAKNRDUDKVIWVPSRKVKPDI:QKDEVTKDEASPL
FAGSDWLPWGEQGLQBEAASNKQGPQEDFLAANES"
6961..7040
/rpt_type=direct
repeat_region
7300..8908
/gene="src"
7300..8907

```

```

/gene="src"
/codon_start=1
/product="src tyrosine kinase"
/protein_id="AAC08990.1"
/db_xref="GI:3003004"
/translocation="MGSSKSKPKDPSHRRSRLEPPDSTHGGPFPASQTNKTAAPDTH
KTPSRSGTVATEPKLFGDNTSDTVSPORAGALAGSVITFVALYDYESWLETDLSP
KXGERLQIVNNTGNNWLAHSTVTGTQGYIPSNYVAPSDSIQABEYFKITRRESR
LLANPENRGTFLVRESSTTKGACLSVDFONAKLNVKHYKIRLSDSGSYITISRT
QFSSLOQLVAYSKHADGLCHRLNVCPSTKQTOGLAKDAWEIPRESLRLEKLGOG
CFGEVWMTWNGCTRVGTWNGCTEVAIKLKPQTSPEAF:QEAOMVKLRHEKULQV
YAVSBEPIYIVIEYMSKSSLLDPLKMGKYLRLPOLVDMAGLIASGMAYVERNVY
HEDLRANILVGNVCKVADFGIARLLEENETTRQAKPEPKIWKIAPAPALIGPFI
KDDVMSFGILLTELTTKGRMPYPMGNGEVLDRVERGYRMECPPECPESLHDMCQCW
REDPEPTEPEYLQALLPACVLEAF"
9002..9096
/rpt_type=direct
LTR
9131..9396
repeat_region
9131..9375
/nc="U3"
9369..9374
polyA_signal
9376..9396
repeat_region
/nc="R"

ORIGIN
Query Match      87.7%; Score 458.6; DB 14; Length 9396;
Best Local Similarity 95.2%; Pred. No. 1.5e-128;
Matches 500; Conservative 0; Mismatches 9; Indels 16; Gaps 2;

Qy      1  CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60
Db      8872 CTGCTCCCTGCTGTGTGTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 8931

Qy      61  ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGCTTAGCGCTTTTGG 120
Db      8932 ACAAGCAAGGCTTGCGCGCAATTCATGAAGAATCTGCTTAGGCTTAGCGCTTTTGG 8991

Qy      121  CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTCTTAG 180
Db      8992 CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTCTTAG 9051

Qy      181  CGAAAAGCGGGCTTCGCTGTACGGGTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240
Db      9052 CGAAAAGCGGGCTTCGCTGTACGGGTAGGAGTCCCTCAGGATATAGTAGTTTCGC 9111

Qy      241  TTTTGCATAGGAGGGGGAATAGTCTTATGCAATATCTCTTAGTAGTCTTGCACATG- 299
Db      9112 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATATCTCTTAGTAGTCTTGCACATGC 9171

Qy      300  ----GTHACGATGAGTTAGCAATGCTCCTACAGGAGAGAGAAAAGCCCGTCATGCG 355
Db      9172 TTATGTAACGATGCTTAGCAACATGCTTATAGGAGAGAGAAAAGCCCGTCATGCG 9231

Qy      356  ATTGGTGGAAAGTAAG-----GTGGTACGATCGTCCCTTATAGGAAGCAACAG 404
Db      9232 ATTGGTGGAGTAAGGTGGTATGATCGTGTATGATGCTGCTTGTAGGAAGCAACAG 9291

Qy      405  ACGGCTCTGACATGAGATTGGACGACCACTAATATCCGATTCAGAGATATTGTATTA 464
Db      9292 ACGGCTCTAACAGGATTGGACCAACCACTGAATTCGCGATTTCAGAGATATTGTATTA 9351

Qy      465  AGTGCCTAGCTGATACATAAAGCCATTTGACCATTCACCACA 509
Db      9352 AGTGCCTAGCTGATACATAAAGCCATTTGACCATTCACCACA 9396

RESULT 68
REASVS
LOCUS
DEFINITION Avian sarcoma virus src gene and part of the env gene.
ACCESSION V01169
VERSION V01169.1 GI:61498
KEYWORDS oncogene.

```



SOURCE Avian sarcoma virus  
ORGANISM Avian sarcoma virus  
REFERENCE 1 (bases 1 to 3107)  
AUTHORS Czerminofsky, A.P., Levinson, A.D., Varmus, H.E., Bishop, J.M.,  
Tischer, E. and Goodman, H.M.  
TITLE Nucleotide sequence of an avian sarcoma virus oncogene (src) and  
proposed amino acid sequence for gene product  
JOURNAL Nature 287 (5779), 198-203 (1980)  
MEDLINE 81052295  
PUBMED 6253794  
REFERENCE 2 (bases 1 to 3107)  
AUTHORS Czerminofsky, A.P., Levinson, A.D., Varmus, H.E., Bishop, J.M.,  
Tischer, E. and Goodman, H.  
TITLE Corrections to the nucleotide sequence of the src gene of Rous  
sarcoma virus  
JOURNAL Nature 301 (5902), 736-738 (1983)  
MEDLINE 83141780  
PUBMED 6298633  
REFERENCE 3 (bases 1 to 3107)  
AUTHORS Czerminofsky, A.P.  
TITLE Direct Submission  
JOURNAL Submitted (15-MAR-1983)  
COMMENT Contains corrections to the original sequence published in [1].  
FEATURES  
source  
1. .3107  
/organism="Avian sarcoma virus"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:11876"  
1. .743  
/gene="env"  
1. .743  
/gene="env"  
/codon\_start=3  
/protein\_id="CAA24494.1"  
/db\_xref="GI:809071"  
/db\_xref="GOA:P03397"  
/translation="IPSPVGPVCLGKLMAPKHTDILKLVNSRTGIRKRST  
LDDTSIRHVALONRAIDFLLAHGSCEDVAGCCNLSQDSSEIQQKFLMKRHHV  
NKGVDLSLIGSWRLGFGIGENAVHLKLLGLVILLVCLPCLQLMLCGNR  
KMNNSISHTPEYKLLQCKAQGPESRV"  
1123. .2703  
/gene="src"  
1123. .2703  
/gene="src"  
/codon\_start=1  
/protein\_id="CAA24495.1"  
/db\_xref="GI:61499"  
/db\_xref="GOA:P00524"  
/db\_xref="SWISS-PROT:P00524"  
/translation="MSSSKPKPPSRRSLRPPDSTHGGPPASQTPNKTAAPDTH  
RTPSPSFWATPKLPFGFNSTVTSRQAGALAGVTVFVALVDYSEWLETLSP  
KGERLQIVNTGKWLVAHSITGQGYIPSNVAPSDSQAENWFKLIRRSER  
LLINPENPGRFVRSSETTKGAYCLVSDFDNAGLVNKHVKIRKLDGSGFYTSRT  
QFSSQQLVAYIKHAGDGLCHRLTNVCPSTPQGLAKDAWEIPRESLRLVLEKLGQ  
CFGEVWMTGTRVAIKTLKPTGSPFAFLQEAQWKLREKLVQLYAVVSEPI  
YIVIEYMSKGLLDLTKGEMGKYLRLPOLVMAAQIAGSMVAVVMNMYHRLRAANI  
LVGENLCKVADGLARLLEDNEXYTAQGAQKFPKWTAPKALYGRFTIKSDVWFSFI  
LLETITKGRVPFPMGNGEVLDRVERGYMPCEPCPESLHDLMLCQWRDPERPT  
FYLQALLPACVLEAE"

Query Match 82.9%; Score 433.6; DB 14; Length 3107;  
Best Local Similarity 99.1%; Pred. No. 6.1e-121;  
Matches 436; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
2668 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 2727  
Db 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
Qy 61 ACAAGGCAAGGCTTACCGCAGCAATTCATGAAGAATCTGCTTAGGCTTTAGCGTTTGGC 120

Db 2728 ACAAGGCAAGGCTTACCGCAGCAATTCATGAAGAATCTGCTTAGGCTTAGCGTTTGGC 2787  
Qy 121 CTGCTTCCGATGTAGCGGACAGATATTCGGTATCTAGCGGAGCTAGGCTGTGTAGG 180  
Db 2788 CTGCTTCCGATGTAGCGGACAGATATTCGGTATCTAGCGGAGCTAGGCTGTGTAGG 2847  
Qy 181 CGAAAAGCGGGGCTTCGGTGTAGCGGCTTAGGAGTCCCTTCAGGATATAGTAGTTTGGC 240  
Db 2848 CGAAAAGCGGGGCTTCGGTGTAGCGGCTTAGGAGTCCCTTCAGGATATAGTAGTTTGGC 2907  
Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTGTGTAGTTCGCAACATGG 300  
Db 2908 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTGTGTAGTTCGCAACATGG 2967  
Qy 301 TAAAGATGAGTATAGCAATGCTTACAGGAGAGAAAAGCACCGCTGCATCGCATGG 360  
Db 2968 TAAAGATGAGTATAGCAATGCTTACAGGAGAGAAAAGCACCGCTGCATCGCATGG 3027  
Qy 361 TGGAGTAAAGTGTACGATCGCTTATAGGAGGCAACAGACGCGTCTGACATGGA 420  
Db 3028 TGGAGTAAAGTGTACGATCGCTTATAGGAGGCAACAGACGCGTCTGACATGGA 3087  
Qy 421 TTGACGAAACCACTAAATC 440  
Db 3088 TTGACGAAACCACTAAATC 3107  
RESULT 69  
XXU02432 8413 bp DNA circular SYN 29-JAN-1997  
DEFINITION Cloning vector pMAMneo, complete sequence.  
ACCESSION U02432  
VERSION U02432.1 GI:413798  
KEYWORDS Cloning vector pMAMneo  
SOURCE Cloning vector pMAMneo  
ORGANISM artificial sequences; vectors.  
REFERENCE 1 (bases 1 to 8413)  
AUTHORS Kitts, P.A.  
TITLE ClONTECH Vectors On Disc version 1.3  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 8413)  
AUTHORS Kitts, P.A.  
TITLE Direct Submission  
JOURNAL Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,  
1020 East Meadow Circle, Palo Alto, CA 94303 USA  
COMMENT This vector can be obtained from CLONTECH Laboratories, Inc., 1020  
East Meadow Circle, Palo Alto, CA 94303, USA. To place an order  
call (415) 424-8222 or (800) 662-2566, extension 1. International  
customers, please contact your local distributor. For technical  
information, call (415) 424-8222 or (800) 662-2566, extension 3.  
This sequence has been compiled from information in the sequence  
databases, published literature and other sources, together with  
partial sequences obtained by CLONTECH; this vector has not been  
completely sequenced. If you suspect there is an error in this  
sequence, please contact CLONTECH's Technical Service Department at  
(415) 424-8222 or (800) 662-2566, extension 3 or E-mail  
TECH@CLONTECH.COM.  
FEATURES  
source  
1. .8413  
/organism="Cloning vector pMAMneo"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31818"  
ORIGIN  
Query Match 82.4%; Score 430.8; DB 12; Length 8413;  
Best Local Similarity 99.5%; Pred. No. 4.4e-120;  
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
Db 2788 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 8039

Qy	121	CTCTTCGCGATGTACGGCCGACAGATCTTCGGCGTATCTGAGGGGACCTAGGCTGTGTTAGG	180
Db	8162	CTGCTTCGCGATGTACGGGCCGACATATACGCGTATCTGAGGGGACCTAGGCTGTGTTAGG	8221
Qy	181	CGAAAAGCGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC	240
Db	8222	CGAAAAGCGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC	8281
Qy	241	TTTTTCGATAGGAGGGGGAATGTAGTCTTATGCAATACTCTTGTAGTCTTGTGCACATGG	300
Db	8282	TTTTTCGATAGGAGGGGGAATGTAGTCTTATGCAATACACTTGTAGTCTGTGCACATGG	8341
Qy	301	TAACGATGAGTTAGCAACATGCTCTTAAGGAGAGAAAAGCACCGTGCATGCCGATGG	360
Db	8342	TAACGATGAGTTAGCAACATGCTCTTAAGGAGAGAAAAGCACCGTGCATGCCGATGG	8401
Qy	361	TGGAAGTAAAGTGTCACGATCGTCCTTATTAGGAGGGCAACAGACGGGTCTGCATGGA	420
Db	8402	TGGAAGTAAAGTGTCACGATCGTCCTTATTAGGAGGGCAACAGACGGGTCTGCATGGA	8461
Qy	421	TTGGACGAACCACT	434
Db	8462	TTGGACGAACCACT	8475

RESULT 71  
XXU02431  
LOCUS  
XXU02431 9184 bp DNA circular SYN 29-JAN-1997  
DEFINITION  
Cloning vector pMAMneo-CAT, complete sequence.

002431	GI:413797	
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		

```
FEATURES
    source
        location/Qualifiers
            1..9184
                /organism="Cloning vector pMAMneo-CAT"
                /mol_type="genomic DNA"
                /db_xref="taxon:31819"
```

ORIGIN	/db_xref="taxon:31819"			
Query Match	82.4%	Score 430.8;	DB 12;	Length 9184;
Best Local Similarity	99.5%;	Pred. No. 4.4e-120;		
Matches 432;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	CTGCTCCCTGCTTGTGTGTGGAGTCCCTGACTAGTCGGGAGCAAAATTTAAGCTACA	60	
Db	8751	CTGCTCCCTGCTTGTGTGTGGAGTCCCTGACTAGTCGGGAGCAAAATTTAAGCTACA	8810	
QY	61	ACAAGGCAAGGGTTGACCGCAATTGCATGAGAATCTGCTTAGGGTTAGGCGTTTTGGC	120	

```

Db      8811  ACAAGGCAAGGCTTGACCGACAAATTGCATGAAGAAATCTGCTTAGGGTTAGGCGTTTTCGC 8870
QY      121  CTGCTTCGCGATGTACGGCGCAGATATTTCGCGTATCTGAGCGGACTAGGCTGTGTTTAGG 180
Db      8871  CTGCTTCGCGATGTACGGCGCAGATATTTCGCGTATCTGAGCGGACTAGGCTGTGTTTAGG 8930
QY      181  CGAAAAGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC 240
Db      8931  CGAAAAGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC 8990
QY      241  TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 300
Db      8991  TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 9050
QY      301  TACCATGAGTTAGCACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360
Db      9051  TACCATGAGTTAGCACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 9110
QY      361  TGGAAATAGGTGATCGATCGCTGCTTATTAGGAAGGCAACAGACGGGTCTGCATGGA 420
Db      9111  TGGAAATAGGTGATCGATCGCTGCTTATTAGGAAGGCAACAGACGGGTCTGCATGGA 9170
QY      421  TTGGACGAACCACT 434
Db      9171  TTGGACGAACCACT 9184

```

```

RESULT 72
LOCUS    U02448                      10339 bp    DNA    circular SYN 29-MAR-1996
DEFINITION Cloning vector pMAMneo-LUC, complete sequence.
ACCESSION U02448
VERSION   U02448.1 GI:413814
KEYWORDS
SOURCE    Cloning vector pMAMneo-LUC
ORGANISM  Cloning vector pMAMneo-LUC
REFERENCE 1 (bases 1 to 10339)
AUTHORS   Kitts, P.A.
TITLE     CLONTECH Vectors On Disc version 1.3
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 10339)
AUTHORS   Kitts, P.A.
TITLE     Direct Submission
JOURNAL   Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
          1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT   In reference 2, this vector is referred to as pBSpac delta P. This
          vector can be obtained from CLONTECH Laboratories, Inc., 1020 East
          Meadow Circle, Palo Alto, CA 94303, USA. To place an order call
          (415) 424-8222 or (800) 662-2566, extension 1. International
          customers, please contact your local distributor. For technical
          information, call (415) 424- 8222 or (800) 662-2566, extension 3.
          This sequence was compiled by Susana de la Luna. If you suspect
          there is an error in this sequence, please contact CLONTECH's
          Technical Service Department at (415) 424-8222 or (800) 662-2566,
          extension 3 or E-mail TECH@CLONTECH.COM.

```

```

FEATURES             Source
    source            1. 10339
                        /organism="Cloning vector pMAMneo-LUC"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:31820"

```

```

ORIGIN
Query Match      82.4%; Score 430.8; DB 12; Length 10339;
Best Local Similarity 99.5%; Pred. No. 4.4e-120;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1  CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db      9906 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 9965
QY      61  ACAAGGCAAGGCTTGACCGACAAATTCGATGAAGAAATCTGCTTAGGGTTAGGCGTTTTCGC 120

```

```

Db      9966  ACAAGGCAAGGCTTGACCGACAAATTCGATGAAGAAATCTGCTTAGGGTTAGGCGTTTTCGC 10025
QY      121  CTGCTTCGCGATGTACGGCGCAGATATTTCGCGTATCTGAGCGGACTAGGCTGTGTTTAGG 180
Db      10026 CTGCTTCGCGATGTACGGCGCAGATATTTCGCGTATCTGAGCGGACTAGGCTGTGTTTAGG 10085
QY      181  CGAAAAGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC 240
Db      10086  CGAAAAGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC 10145
QY      241  TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 300
Db      10146  TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGCACATGG 10205
QY      301  TACCATGAGTTAGCACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360
Db      10206  TACCATGAGTTAGCACATGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 10265
QY      361  TGGAAATAGGTGATCGATCGCTGCTTATTAGGAAGGCAACAGACGGGTCTGCATGGA 420
Db      10266  TGGAAATAGGTGATCGATCGCTGCTTATTAGGAAGGCAACAGACGGGTCTGCATGGA 10325
QY      421  TTGGACGAACCACT 434
Db      10326  TTGGACGAACCACT 10339

```

```

RESULT 73
LOCUS    BD268238                      11600 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION Adenovirus vector, packaging cell line, composition and method for
          production and use.
ACCESSION BD268238
VERSION   BD268238.1 GI:33078006
KEYWORDS  JP 2002534130-A/42.
SOURCE    synthetic construct
ORGANISM  synthetic construct
REFERENCE 1 (bases 1 to 11600)
AUTHORS   Nemerow, G.R., Seggern, D.J.V., Hallenbeck, P.L., Stevenson, S.C. and
          Skripchenko, Y.
TITLE     Adenovirus vector, packaging cell line, composition and method for
          production and use
JOURNAL   Patent: JP 2002534130-A 42 15-OCT-2002;
          NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
COMMENT   OS Artificial Sequence
          PN JP 2002534130-A/42
          PD 15-OCT-2002
          PF 14-JAN-2000 JP 2000593765
          PI 14-JAN-1999 US 60/115920
          PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI
          SUSAN C STEVENSON, YELENA SKRIPCHENKO
          PC C12N15/09, A61K35/76, A61P43/00, A61P35/00, A61P43/00, A61P43/00,
          PC C12N5/10,
          PC C12N7/00, C12Q1/68, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
          Description of Artificial Sequence: plasmid
          FH Key Location/Qualifiers
          FT source 1. 11600
                        /organism='Artificial Sequence'

```

```

FEATURES             Location/Qualifiers
    source            1. 11600
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

```

```

ORIGIN
Query Match      82.4%; Score 430.8; DB 6; Length 11600;
Best Local Similarity 99.5%; Pred. No. 4.5e-120;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1  CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db      11167 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 11226

```

```

QY 61 ACAGCAAGGCTTACCGCAATTCGATGAGAACTCTCTAGGTTAGCGTTTTCG 120
Db 11227 ACAAGCAAGGCTTACCGCAATTCGATGAGAACTCTCTAGGTTAGCGTTTTCG 11286
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGCACTAGGGTGTGTTAG 180
Db 11287 CTGCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGCACTAGGGTGTGTTAG 11346
QY 181 CGAAAGCGGGCTTCGCTTGTACGGGTTAGGAGTCCCTCAGGATATAGTTTTCG 240
Db 11347 CGAAAGCGGGCTTCGCTTGTACGGGTTAGGAGTCCCTCAGGATATAGTTTTCG 11406
QY 241 TTTTGCATAGGAGGGGAAATAGTAGTCTTATGCAATCTCTTGTAGTCTTGAACATGG 300
Db 11407 TTTTGCATAGGAGGGGAAATAGTAGTCTTATGCAATCTCTTGTAGTCTTGAACATGG 11466
QY 301 TAACGATAGTTAGCAATCGCTTACAGGAGAGAAAGCACCGTGCATGCCGATTGG 360
Db 11467 TAACGATAGTTAGCAATCGCTTACAGGAGAGAAAGCACCGTGCATGCCGATTGG 11526
QY 361 TGAAGTAAAGTGTGATCGTGTCTTATGAGGAGCAACAGCGGCTCTGACATGA 420
Db 11527 TGAAGTAAAGTGTGATCGTGTCTTATGAGGAGCAACAGCGGCTCTGACATGA 11586
QY 421 TTGACGACCACT 434
Db 11587 TTGACGACCACT 11600

RESULT 74
RSU41727 874 bp DNA linear VRL 18-JUL-2001
LOCUS Rous sarcoma virus Schmidt-Ruppin subgroup A (NY) clone iPH2013-4,
DEFINITION Sp37 (env) gene, partial cds, and 3'/LTR.
ACCESSION U41727
VERSION U41727.1 GI:1136589
KEYWORDS
SOURCE Rous sarcoma virus
ORGANISM Rous sarcoma virus
REFERENCE 1 (bases 1 to 532)
AUTHORS Hara.H. and Kaji.A.
TITLE The U3 region of the long terminal repeat of a subgroup A
transformation-defective rous sarcoma virus (tdPH2010) converts a
necropathic virus to a cytopathic virus
JOURNAL Virus Genes 15 (2), 171-180 (1997)
MEDLINE 98083689
PUBMED 9421881
REFERENCE 2 (bases 1 to 874)
AUTHORS Hara.H.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1995) Hiroto Hara, University of Pennsylvania
School of Medicine, Microbiology, 573 Maloney Building, 36th and
Spruce Street, Philadelphia, PA 19104-4283, USA
FEATURES
source
1. 874
/organism="Rous sarcoma virus"
/proviral
/mol_type="genomic DNA"
/strain="Schmidt-Ruppin subgroup A (NY)"
/species_host="Gallus gallus"
/db_xref="taxon:11886"
/clone="lambda iPH2013-4"
/lab_host="Gallus gallus"
1. .35
/gene="env"
<1. .35
/gene="env"
/function="envelope transmembrane protein"
/codon_start=3
/product="gp37"
/protein_id="AAB60581.1"

```

```

/db_xref="GI:1136590"
/translation="AYQPEPRIV"
76. .191
/note="direct; drl (left)"
372. .373
/note="src deletion site"
/organism="Rous sarcoma virus"
414. .533
/note="direct; drl (right)"
542. .874
/note="3' LTR"
542. .775
/note="U3"
misc_difference 650
/note="T in transformation-defective, cytopathic strain
tdPH2010"
/misc_difference 753
/note="A in transformation, cytopathic strain tdPH2010"
/repeat_unit 776. .796
/note="R"
797. .874
/note="U5"
ORIGIN
Query Match 78.4%; Score 409.8; DB 14; Length 874;
Best Local Similarity 97.3%; Pred. No. 1.1e-113;
Matches 429; Conservative 0; Mismatches 7; Indels 5; Gaps 1;
QY 87 CATGAGAAATCTCTAGGGTTAGGCGTTTTCGCTCTTCGCGATGACGGCCAGATA 146
Db 369 CGTAAAGAAATCTCTAGGGTTAGGCGTTTTCGCTCTTCGCGATGACGGCCAGATA 428
QY 147 TTCGCTATCTGAGGAGCTAGGCTGTGTTAGGCGAAAGCGGGCTTCGTTGTACGC 206
Db 429 TACGTGTATCTGAGGAGCTAGGCTGTGTTAGGCGAAAGCGGGCTTCGTTGTACGC 488
QY 207 GGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGAAATAG 266
Db 489 GGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGAAATAG 548
QY 267 TCTTATGCAATCTCTTGTAGTCTTGCACATG-----GTAACGATGAGTTAGCAATG 321
Db 549 TCTTATGCAATCTCTTGTAGTCTTGCACATGCTTATGTAACGATGAGTTAGCAATG 608
QY 322 CTTTACAGGAGGAGAAAGCAACCGTGCATGCCGATGTTGGAAGTAAGGTGTACCATC 381
Db 609 CTTTACAGGAGGAGAAAGCAACCGTGCATGCCGATGTTGGAAGTAAGGTGTACCATC 668
QY 382 GTGCTTTATTAGGAGGCAACAGACGCGTCTGCATGCGATTGGACCAACCACTAATTC 441
Db 669 GTGCTTTATTAGGAGGCAACAGACGCGTCTGCATGCGATTGGACCAACCACTAATTC 728
QY 442 GCATTGAGAGATATTGATTTAGTCCCTAGCTCGATACATTAACGCGCATTTGACCAT 501
Db 729 GCATTGAGAGATATTGATTTAGTCCCTAGCTCGATACATTAACGCGCATTTGACCAT 788
QY 502 TCACCACTTTGTTGTCACCT 522
Db 789 TCACCACTTTGTTGTCACCT 809

RESULT 75
BD268239 8238 bp DNA linear PAT 17-JUL-2003
LOCUS Adenovirus vector, packaging cell line, composition and method for
DEFINITION production and use.
ACCESSION BD268239
VERSION BD268239.1 GI:33078007
KEYWORDS JP 2002534130-A/43.
SOURCE synthetic construct
ORGANISM synthetic construct

```

artificial sequences.  
1 (bases 1 to 8238)  
REFERENCE Nemerow, G.R., Seggern, D.J.V., Hallenbeck, P.L., Stevenson, S.C. and  
AUTHORS Skripchenko, Y.  
TITLE Adenovirus vector, packaging cell line, composition and method for  
JOURNAL production and use  
COMMENT Patent: JP 2002534130-A 43 15-OCT-2002;  
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE  
OS Artificial Sequence  
PN JP 2002534130-A/43  
PD 15-OCT-2002  
PF 14-JAN-2000 JP 2000593765  
PR 14-JAN-1999 US 60/115920  
PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI  
SUSAN C STEVENSON, YELENA SKRIPCHENKO  
PC C12N15/09, A61K35/76, A61K48/00, A61P35/00, A61P43/00, A61P43/00,  
PC C12N5/10, C12N1/69, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC  
PC C12N7/00, C12N1/69, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC  
Description of Artificial Sequence: plasmid  
FH Key Location/Qualifiers  
FT source 1..8238  
FT /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..8238  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 75.1%; Score 393; DB 6; Length 8238;  
Best Local Similarity 98.8%; Pred. No. 1.5e-108;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 123 GCTTCCGATGTACGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
Db 404 GCGCCCGGATGTACGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGGCG 463  
QY 183 AAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
Db 464 AAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 523  
QY 243 TTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGGA 302  
Db 524 TTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGGA 583  
QY 303 ACATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCAGCGTCATGCCGATTGGTG 362  
Db 584 ACATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCAGCGTCATGCCGATTGGTG 643  
QY 363 GAAGTAAGTGTGTACGATCGTCTTATTAGGAGGCAAGACAGCGGTTGACATGATT 422  
Db 644 GAAGTAAGTGTGTACGATCGTCTTATTAGGAGGCAAGACAGCGGTTGACATGATT 703  
QY 423 GGACGACCACTAATTCGCTATTCGAGATATTTATTAGTGCCTAGCTCGATACA 482  
Db 704 GGACGACCACTAATTCGCTATTCGAGATATTTATTAGTGCCTAGCTCGATACA 763  
QY 483 ATAAAGCCATTGACCAATTCACCACTTGGTGTGACCTC 523  
Db 764 ATAAAGCCATTGACCAATTCACCACTTGGTGTGACCTC 804

Search completed: March 11, 2004, 09:42:27  
Job time : 2938.11 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 03:02:06 ; Search time 451.626 Seconds  
(without alignments)  
4919.575 Million cell updates/sec

Title: US-09-733-368a-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgtctccgttggtgttt.....accacattgtgtgcacctc 523

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : N Geneseq\_29Jan04.\*

- 1: geneseqn1980s.\*
- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002s.\*
- 7: geneseqn2003as.\*
- 8: geneseqn2003bs.\*
- 9: geneseqn2003cs.\*
- 10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523	100.0	648	4	Aah43951 Rous sarc
2	519.8	99.4	7086	9	Adh35600 Tricistron
3	517.8	99.0	2245	7	Abz23249 Lac repre
4	515	98.5	4965	2	Aag75973 pHLA-B*7/b
5	513.8	98.2	562	7	Abz23250 Nucleotid
6	508.8	97.3	4457	9	Adh35599 Bicistron
7	508.8	97.3	7334	9	Adh35601 Tetractist
8	505.6	96.7	4059	2	Aag75974 pHLA-B*7 e
9	505.6	96.7	4341	6	Aag62391 Vector pv
10	505.6	96.7	4341	6	Aas17704 Vector pv
11	505.6	96.7	4341	6	Adh83143 Plasmid p
12	505.6	96.7	5653	2	Aat02998 RSV tar R
13	505.6	96.7	5653	2	Aat76802 RSV tar R
14	505.6	96.7	5750	2	Aa043814 pRLD3D4 C
15	505.6	96.7	6207	2	Aa043813 pRLD3D4 C
16	505.6	96.7	6274	2	Aa043812 pRLD1D2D3
17	505.6	96.7	8591	2	Aat84562 Plasmid p
18	505.6	96.7	8591	2	Aat84561 Plasmid p
19	505.6	96.7	8591	2	Aat87083 Plasmid p
20	505.6	96.7	8591	2	Aat87084 Plasmid p
21	505.6	96.7	8591	2	Aav04866 cDNA enco
22	505.6	96.7	8591	2	Aav04865 cDNA enco
23	505.6	96.7	8591	2	Aav05850 APP-REP 7

Aav05849 APP-REP 7  
Aat62602 Luciferas  
Aas53869 Expressio  
Abl57333 Vector pl  
Aas53873 Expressio  
Aas53879 Expressio  
Aas53875 Expressio  
Aas53874 Expressio  
Aas53876 Expressio  
Aat71261 Rous sarc  
Aaz60824 Nucleotid  
Aas59077 Nucleotid  
Aba94279 Nucleotid  
Aal56865 DNA seque  
Adb75125 Chromosom  
Aal14722 Nucleotid  
Aaz93333 Partial s  
Aaz93078 Partial s  
Aaz93331 Partial s  
Aaz93079 Partial s  
Aac89169 AdRSVpHYD  
Aaa09085 AdRSV-bet  
Aaa59078 Nucleotid  
Aal56867 DNA seque  
Aaz94163 Adenoviru  
Aal56866 DNA seque  
Aaz29699 Viral exp  
Aal55269 DNA of ex  
Aaz94161 395 Nucle  
Aal14719 Nucleotid  
Aaz93077 Rous Sarc  
Aax02780 Vector pM  
Aaz02997 Bovine sc  
Aad28272 LSRNL vec  
Aad28311 LSRNL vec  
Aas15665 Human res  
Aaq06310 Sequence  
Aaq06311 Sequence  
Aaq06309 Sequence  
Aaq06313 Sequence  
Aaq06312 Sequence  
Aad27899 pMT2 vec  
Aac92489 Fragment  
Aax77359 Polynucle  
Aaa90391 987Bbreo  
Aaz27850 Complete  
Aad04741 Alphavira  
Aaf84024 Complete  
Abx10062 Expressio  
Aad53272 MSV2/EGF  
Aad53270 MSV2/ACT  
Aad53271 MSV2/IRE  
Aad14296 MSV2/EGF  
Aad13899 Recombina  
Aad53274 MSV2/EGF  
Aad53290 MSV2/EGF  
Aad53293 MSV2/EGF  
Aad53292 MSV2/EGF  
Aad53273 MSV2/EGF  
Aad53289 MSV2/EGF  
Aad53291 MSV2/EGF  
Aad14199 MSV2/EGF  
Aad14203 MSV2/EGF  
Abl90071 Human pol  
Aav58058 Plasmid C  
Aad02037 Plasmid p  
Aad02036 Plasmid p  
Aac62937 3F4 human  
Aat62932 2A2 human  
Aav40006 Plasmid p  
Aat90695 Plasmid C  
Aav40007 Plasmid p

97 151.4 28.9 4249 2 AAV63466 Plasmid p  
98 151.4 28.9 4597 4 AAF24901 Nucleotid  
99 151.4 28.9 4840 4 AAF83146 Complete  
100 151.4 28.9 5015 9 ADB33528 Expressio

ALIGNMENTS

RESULT 1  
AAH43951  
ID AAH43951 standard; DNA; 648 BP.  
XX  
AC AAH43951;  
XX  
DT 06-SEP-2001 (first entry)  
XX  
DE Rous sarcoma virus promoter nucleotide sequence SEQ ID NO:1.  
XX  
KW Rous sarcoma virus; promoter; enhancer; RSV; primate; gene expression;  
KW transgene; genetic engineering; gene therapy; immunisation; ds.  
XX  
OS Rous sarcoma virus.  
XX  
PN WO200142444-A2.  
XX  
PD 14-JUN-2001.  
XX  
PF 08-DEC-2000; 2000WO-US033256.  
XX  
PR 10-DEC-1999; 99US-0170019P.  
XX  
PA (ARIA-) ARIAD GENE THERAPEUTICS INC.  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Rivera V, Zolnick P, Wilson JM;  
XX  
XX WPI; 2001-381673/40.  
XX  
XX Genetically engineering a primate for expression of a desired gene,  
PT comprises introducing into the primate a transgene comprising Rous  
PT Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to  
PT RSV promoter.  
XX  
XX Claim 7; Page 44; 64pp; English.  
XX  
CC The present invention describes a method for genetically engineering a  
CC primate for expression of a desired gene comprising introducing into the  
CC primate a transgene comprising an Rous Sarcoma Virus (RSV) promoter and a  
CC nucleic acid sequence heterologous to RSV promoter. Also described is a  
CC primate cell (i) containing and capable of expressing a transgene  
CC comprising an RSV promoter operably linked to a recombinant nucleic acid  
CC encoding one or more fusion proteins, where the fusion proteins bind to a  
CC ligand and in the presence of the ligand modulate(s) the expression level  
CC of a target gene. The method can be used for high level expression of  
CC genes in primates or for engineering primate cells. It is useful for  
CC increasing the efficacy of many gene therapy strategies, and for  
CC increasing the efficacy of intracellular immunisation agents, molecules  
CC like ribozymes, antisense RNA, and dominant negative proteins, that act  
CC either stoichiometrically, or by competition. The method increases the  
CC efficacy of many gene therapy strategies by substantially elevating the  
CC expression of an exogenous therapeutic gene, and allowing expression to  
CC reach therapeutically effective levels. The present sequence represents a  
CC specifically claimed RSV enhancer/promoter nucleotide sequence from the  
CC present invention  
XX  
XX Sequence 648 BP; 163 A; 135 C; 179 G; 171 T; 0 U; 0 Other;  
SQ

Query March 100.0%; Score 523; DB 4; Length 648;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGGAGGTCGTGAGTAGTCGGCGGACCAAAATTTAGCTACA 60

Db 90 CTGCTCCCTGCTGTGTGTGGAGGTCGTGAGTAGTCGGCGGACCAAAATTTAGCTACA 149  
QY 61 ACAGGCGAAGGCTTCAGCGCAATTCGATGAGGAATCTGCTTAGGCTTAGCGCTTTGGCG 120  
Db 150 ACAAGGCGAAGGCTTCAGCGCAATTCGATGAGGAATCTGCTTAGGCTTAGCGCTTTGGCG 209  
QY 121 CTGCTTCGCGATGTACGGGGCCAGATATTCGCGTATCTAGGGGACTAGGGTGTCTTTAGG 180  
Db 210 CTGCTTCGCGATGTACGGGGCCAGATATTCGCGTATCTAGGGGACTAGGGTGTCTTTAGG 269  
QY 181 CGAAAGCGGGGCTTCGGGTGTACGGGCTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 270 CGAAAGCGGGGCTTCGGGTGTACGGGCTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 329  
QY 241 TTTTGCATAGGGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
Db 330 TTTTGCATAGGGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 389  
QY 301 TAACGATGATGTAGCAACATGCCCTTACAAAGGAGAGAAAAGCAACCGTGATCGCGATGG 360  
Db 390 TAAAGATGATGTAGCAACATGCCCTTACAAAGGAGAGAAAAGCAACCGTGATCGCGATGG 449  
QY 361 TGGAGTGTAGGTGCTACCATCGTCCCTTATTAGGAGGCAACAGCGGCTCTGACATGGA 420  
Db 450 TGGAGTGTAGGTGCTACCATCGTCCCTTATTAGGAGGCAACAGCGGCTCTGACATGGA 509  
QY 421 TTGGACGAACCACTAAATTCGCAATTCGAGAGATATTTAGTGTGCTAGCTCGATA 480  
Db 510 TTGGACGAACCACTAAATTCGCAATTCGAGAGATATTTAGTGTGCTAGCTCGATA 569  
QY 481 CAATPAAAGCCATTTGACCATTCACCATTCACCATTCGCTGTGACCTC 523  
Db 570 CAATPAAAGCCATTTGACCATTCACCATTCACCATTCGCTGTGACCTC 612

RESULT 2  
ADD35600/c  
ID ADD35600 standard; DNA; 7086 BP.  
XX  
AC ADD35600;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Tricistronic eukaryotic expression vector PL249.  
XX  
KW Multicistronic eukaryotic expression vector; multiple protein expression;  
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;  
KW chain terminator; transcription pause site; gene transfer;  
KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;  
KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;  
KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;  
KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;  
KW MRGB terminator; cyclic; circular; ds.  
OS Chimeric.  
OS Synthetic.  
OS Human herpesvirus 5.  
OS Encephalomyocarditis virus.  
OS Simian virus 40.  
OS Rous sarcoma virus.  
OS Oryctolagus cuniculus.  
OS Escherichia coli.  
XX  
XX WO2003031630-A1.  
XX  
XX 17-APR-2003.  
XX  
PF 10-OCT-2002; 2002WO-IT000646.  
XX  
XX 12-OCT-2001; 2001IT-MI002110.  
XX  
XX (KERY-) KERYOS SPA.  
PA

XX Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;  
 PI WPI; 2003-393446/37.  
 DR  
 XX New multicistronic recombinant plasmid vectors expressing two to our  
 PT genes simultaneously, useful in various biotechnological applications,  
 PT such as gene transfer, gene therapy and in DNA immunization.  
 XX  
 PS Claim 18; SEQ ID NO 3; 52pp; English.  
 XX  
 CC The invention relates to multicistronic eukaryotic expression vectors for  
 CC the expression of at least two proteins of interest which may be  
 CC identical or different. The vectors comprise at least one eukaryotic  
 CC expression cassette having a promoter/enhancer sequence, an intron  
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)  
 CC and a chain terminator. The vectors may additionally contain a  
 CC transcription pause site downstream of the chain terminator. The  
 CC invention also encompasses eukaryotic host cells comprising a vector of  
 CC the invention, and the recombinant expression of two or more eukaryotic  
 CC proteins using host cells transformed with a vector of the invention.  
 CC The vectors are useful in various biotechnological applications in which  
 CC the simultaneous expression of two or more genes is necessary, such as  
 CC gene transfer protocols, DNA immunisation, or for the expression of  
 CC different molecules in the same cell. They may also be used in gene  
 CC therapy. The present sequence represents a specifically claimed vector  
 CC designated PL249, which comprises a cytomegalovirus (CMV)  
 CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)  
 CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous  
 CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, and a rabbit  
 CC beta-globin gene mRGE terminator as well as a kanamycin resistance gene.  
 XX  
 SQ Sequence 7086 BP; 1870 A; 1699 C; 1753 G; 1764 T; 0 U; 0 Other;

Query Match 99.4%; Score 519.8; DB 9; Length 7086;  
 Best Local Similarity 99.6%; Pred. No. 8.3e-172;  
 Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTTGGTGGAGTGGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
 Db 2055 CTGCTCCCTGCTGTTGGTGGAGTGGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 1996

Qy 61 ACAAGGCAAGGCTTGCACGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGC 120  
 Db 1995 ACAAGGCAAGGCTTGCACGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGC 1936

Qy 121 CTGCTCCGAGTACGGGCGAGATTCGCGTATCTGAGGGGAGTAGGGTGTGTTAGG 180  
 Db 1935 CTGCTTCGCGATGTACGGGCGAGATATACGGTATCTGAGGGGAGTAGGGTGTGTTAGG 1876

Qy 181 CGAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTGC 240  
 Db 1875 CGAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTGC 1816

Qy 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTTGAGTCTTGAACATGG 300  
 Db 1815 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATATCTTTGAGTCTTGAACATGG 1756

Qy 301 TACGATGAGTACGACATGCTTACAGGAGGAGAAAGCAACGTCATGCCGATTTGG 360  
 Db 1755 TACGATGAGTACGACATGCTTACAGGAGGAGAAAGCAACGTCATGCCGATTTGG 1696

Qy 361 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTTGACATGGA 420  
 Db 1695 TGGAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTTGACATGGA 1636

Qy 421 TTGGAACGACACCAATTAATTCGATTCGACGAGATTTGATTTAAGTCCCTAGCTGATA 480  
 Db 1635 TTGGAACGACACCAATTAATTCGATTCGACGAGATTTGATTTAAGTCCCTAGCTGATA 1576

Qy 481 CAAATTAACGCAATTTGACCAATTCACCAATTTGCTGACCTC 523  
 Db 1575 CAAATTAACGCAATTTGACCAATTCACCAATTTGCTGACCTC 1533

RESULT 3  
 ABZ23249  
 ID ABZ23249 standard; DNA; 2245 BP.  
 XX  
 AC ABZ23249;  
 XX  
 DT 24-MAR-2003 (first entry)  
 XX  
 DE Lac repressor operated p21-expression cassette and RSV-LTR promoter.  
 XX  
 KW Lac repressor; p21; RSV; LTR promoter; cell cycle inhibitor protein;  
 KW protein production; anchorage-independent producer cell line; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT promoter i.563  
 FT /tag= a  
 FT /note= "RSV-LTR promoter"  
 FT intron 564..1051  
 FT /tag= b  
 FT /note= "SV40 small t antigen intron"  
 FT misc\_feature 1052..1907  
 FT /tag= c  
 FT /note= "p21 coding sequence"  
 FT polyA\_signal 1908..2245  
 FT /tag= d  
 FT /note= "thymidine kinase polyA site"  
 XX  
 PN W0200299100-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 03-JUN-2002; 2002WO-EP006054.  
 XX  
 PR 01-JUN-2001; 2001GB-00013318.  
 XX  
 PA (LONZ ) LONZA BIOLOGICS PLC.  
 XX  
 PI Al-Rubeai M, Shuttlesworth J;  
 XX  
 DR WPI; 2003-148669/14.  
 XX  
 PT Producing recombinant protein, particularly for maximizing or enhancing  
 PT e.g. therapeutic protein production, by co-expressing protein with  
 PT recombinant cell cycle inhibitor protein (p21) in producer cell line.  
 XX  
 PS Example 1; Page 15-16; 33pp; English.  
 XX  
 CC The present sequence represents a lac repressor operated p21-expression  
 CC cassette comprising the Rous sarcoma virus (RSV)-LTR promoter. p21 is a  
 CC cell cycle inhibitor protein. The present sequence is used to produce  
 CC vectors for use in the method of the invention. The specification  
 CC describes a method for producing a protein, preferably a recombinant  
 CC protein, in a mammalian anchorage-independent producer cell line. The  
 CC method comprises co-expressing with the protein in the producer cell line  
 CC a recombinant cell cycle inhibitor protein (preferably p21). The method  
 CC is useful for producing a recombinant protein in a producer cell line.  
 CC This is particularly useful for maximizing or enhancing the production of  
 CC e.g. therapeutic proteins at an industrial scale  
 XX  
 SQ Sequence 2245 BP; 532 A; 555 C; 625 G; 533 T; 0 U; 0 Other;

Query Match 99.0%; Score 517.8; DB 7; Length 2245;  
 Best Local Similarity 99.6%; Pred. No. 2.3e-171;  
 Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTTGGTGGAGTGGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
 Db 46 CTGCTCCCTGCTGTTGGTGGAGTGGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 105



```

QY 61 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCGC 120
Db 106 ACAGGCGAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCGC 165
QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGAAGTCTAGGCTGTTTAGG 180
Db 166 CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGAAGTCTAGGCTGTTTAGG 225
QY 181 CGAAGAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGATATAGTATGTTTCGC 240
Db 226 CGAAGAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGATATAGTATGTTTCGC 285
QY 241 TTTTTCATAGGAGGAGGAAATGATCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
Db 286 TTTTTCATAGGAGGAGGAAATGATCTTATGCAATCTCTTGTAGTCTTGCACATGG 345
QY 301 TAACGATGATGTACGACATGCTTACAGGAGAGAGAAAGACCGTGCTAGCGATGG 360
Db 346 TAACGATGATGTACGACATGCTTACAGGAGAGAGAAAGACCGTGCTAGCGATGG 405
QY 361 TGAAGTAAAGTGTACGATCGTGTCTTATTAGGAGGCAACAGACGGGCTCGACATGA 420
Db 406 TGAAGTAAAGTGTACGATCGTGTCTTATTAGGAGGCAACAGACGGGCTCGACATGA 465
QY 421 TTGGACGACACCAATTAATCCGATTCGAGAGATATTGTATTAAAGTCCCTAGCTCGATA 480
Db 466 TTGGACGACACCAATTAATCCGATTCGAGAGATATTGTATTAAAGTCCCTAGCTCGATA 525
QY 481 CATTAACGCCATTGACCATTCACCAATTTGGTGTGCACC 521
Db 526 CATTAACGCCATTGACCATTCACCAATTTGGTGTGCACC 566

RESULT 4
AAQ75973
ID AAQ75973 standard; cDNA; 4965 BP.
XX AC AAQ75973;
XX DT 25-MAR-2003 (revised)
XX DT 23-AUG-1995 (first entry)
XX DE
XX KW expression vector; pHLA-B7/beta-2 microglobulin expression vector.
XX KW light beta-2 microglobulin; heavy human HLA-B7;
XX KW MHC; bicistronic mRNA; human leukocyte antigen; HLA;
XX KW covalently closed circular DNA; ds.
XX OS Synthetic.
XX FH
XX FH Key
XX FH LTR
XX FH Location/Qualifiers
XX FH 1. 529
XX FH /*tag= a
XX FH /note= "Rous sarcoma virus LTR promoter domain, derived
XX FH for the Schmidt-Rupin strain nucleotides 8673-9146. This
XX FH region also includes a 56 bp region of a synthetic
XX FH oligonucleotide which modifies this regulatory sequence
XX FH to effect a higher level of expression of downstream
XX FH sequences. The oligonucleotide removes a polyadenylation
XX FH signal sequence originally found in the RSV DNA
XX FH sequence."
XX FH misc_signal 531..534
XX FH /*tag= b
XX FH /label= consensus_Kozak_signal_sequence
XX FH 535..1620
XX FH /*tag= c
XX FH /note= "HLA-B7 heavy chain open reading frame"
XX FH 535..606
XX FH /*tag= d
XX FH /note= "encodes putative signal peptide of the HLA-B7
XX FH heavy chain"
XX FH 607..1620

/ *tag= e
/ *note= "encodes putative HLA-B7 heavy chain mature
peptide"
1621..1853
/ *tag= f
/ *note= "3' untranslated sequence of HLA-B7 heavy chain
mRNA"
1854..1888
misc_feature
/ *tag= g
/ *note= "multiple cloning site, forms a junction between
the HLA-B7 sequence and the EMCV-CITE sequence, and is
used to facilitate subcloning"
1889..2479
RBS
/ *tag= h
/ *note= "murine encephalomyocarditis CAP-independent
translational enhancer (EMCV-CITE); taken from
nucleotides 255-843 of cloned EMCV genomic DNA. It is a
non-coding regulatory sequence functioning as an internal
entry point for the eukaryotic ribosomal subunits when
located within a mRNA mol. . It enables the translational
start codon of the beta-2 microglobulin, downstream of
the HLA-B7 stop codon on this bicistronic mRNA to be
recognised by the ribosome"
2480..2839
CDS
/ *tag= i
/ *note= "encodes beta-2 microglobulin; this cDNA is deriv.
from chimpanzee (differs to the human cDNA by only 4
bases)"
2840..2846
3'UTR
/ *tag= j
/ *note= "3' untranslated region of the beta-2
microglobulin mRNA"
2847..2870
misc_feature
/ *tag= k
/ *note= "synthetic linker"
2879..2984
polyA_signal
/ *tag= l
3112..3151
misc_feature
/ *tag= m
/ *note= "synthetic linker to facilitate cloning"
complement(3151..3967)
CDS
/ *tag= n
/ *note= "kanamycin resistance gene open reading frame; the
gene is taken from the transposable element Tn903"
4014..4965
misc_feature
/ *tag= o
/ *note= "pBR322 backbone contg. bacterial origin of
replication, it represents nucleotides 2244-3193"

WO9429469-A2.
22-DEC-1994.
94WO-US006069.
27-MAY-1994;
93US-00074344.
07-JUN-1993;
93US-00074344.
(VICA-) VICAL INC.
(UNMI) UNIV MICHIGAN.
Nabel GJ, Nabel EG, Lew D, Marquet M;
WPI; 1995-036494/05.
New vectors for gene therapy, partic for tumours - comprising genetic
material encoding one or more cistron(s) which express immunogenic or
therapeutic peptide(s).
Claim 8; Page 41-42; 50pp; English.
The pHLA-B7/beta-2 microglobulin plasmid expression vector, in addition
to the kanamycin resistance gene, contains the plasmid DNA encoding the
heavy (human HLA-B7) and light (beta-2 microglobulin) proteins of a class

```

CC I major histocompatibility complex (MHC) antigen. The plasmid is  
 CC designed to express these two proteins via a bicistronic mRNA in  
 CC eukaryotic cells. Initiation of transcription of the mRNA is dependent on  
 CC a Rous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long  
 CC terminal repeat. Termination of transcription is dependent upon the  
 CC polyadenylation signal sequence deriv. from the bovine growth hormone  
 CC gene. Eukaryotic cell translation of the heavy chain is regulated by the  
 CC 5' cap-dependent protein start site. Translation of the light chain is  
 CC controlled by the CITE. Finally the replication of the plasmid in  
 CC bacterial cells is controlled by the presence of a bacterial origin of  
 CC replication. The vector is used partic. for the treatment of neoplastic  
 CC disease, eg. melanoma, and provides enhanced gene delivery and expression  
 CC in vivo. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 4965 BP; 1171 A; 1293 C; 1338 G; 1163 T; 0 U; 0 Other;

Query Match 98.5%; Score 515; DB 2; Length 4965;  
 Best Local Similarity 99.0%; Pred. No. 3.4e-170;  
 Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
 Db 1 CTGCTCCCTGCTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
 Qy 61 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
 Db 61 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
 Qy 121 CTGCTTCGGATGTACGGGCGAGATTCGCGGTATCTGAGGGGATAGGGTGTGTTAGG 180  
 Db 121 CTGCTTCGGATGTACGGGCGAGATTCGCGGTATCTGAGGGGATAGGGTGTGTTAGG 180  
 Qy 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGGATATAGTATTTCGC 240  
 Db 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGGATATAGTATTTCGC 240  
 Qy 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Db 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Qy 301 TAACGATAGTTAGCAACATGCTCTACAGGAGGAAAGACACCGTCATGCCGATGG 360  
 Db 301 TAACGATAGTTAGCAACATGCTCTACAGGAGGAAAGACACCGTCATGCCGATGG 360  
 Qy 361 TGGAGTAAAGTGTGATCGATCGCTTATAGGAGGCAACAGACGGCTCTGACATGGA 420  
 Db 361 TGGAGTAAAGTGTGATCGATCGCTTATAGGAGGCAACAGACGGCTCTGACATGGA 420  
 Qy 421 TTGACGAAACCACTAAATTCGCAATTCGAGATATTGTTATTTAAGTGCCTAGCTCGATA 480  
 Db 421 TTGACGAAACCACTAAATTCGCAATTCGAGATATTGTTATTTAAGTGCCTAGCTCGATA 480  
 Qy 481 CAATAAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 481 CTCTAGACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523

RESULT 5  
 ABZ23250  
 ID ABZ23250 standard; DNA; 562 BP.  
 XX AC  
 XX ABZ23250;  
 XX AC  
 XX 24-MAR-2003 (first entry)  
 XX DE Nucleotide sequence of the Rous sarcoma virus (RSV)-LTR promoter.  
 XX KW p21; RSV; LTR promoter; cell cycle inhibitor protein; protein production;  
 XX KW anchorage-independent producer cell line; ss.  
 XX OS Rous sarcoma virus.  
 XX FN W0200299100-A2.

XX 12-DEC-2002.  
 XX 03-JUN-2002; 2002WO-EP006054.  
 XX 01-JUN-2001; 2001GB-00013318.  
 XX (LONZ ) LONZA BIOLOGICS PLC.  
 XX Al-Rubeai M, Shuttleworth J;  
 XX WPI; 2003-148669/14.  
 XX Producing recombinant protein, particularly for maximizing or enhancing  
 XX e.g. therapeutic protein production, by co-expressing protein with  
 XX recombinant cell cycle inhibitor protein (p21) in producer cell line.  
 XX Disclosure; Page 32-33; 33pp; English.  
 XX The present sequence represents the Rous sarcoma virus (RSV)-LTR  
 XX promoter. The present sequence is used to produce vectors for use in the  
 XX method of the invention. The specification describes a method for  
 XX producing a protein, preferably a recombinant protein, in a mammalian  
 XX anchorage-independent producer cell line. The method comprises co-  
 XX expressing with the protein in the producer cell line a recombinant cell  
 XX cycle inhibitor protein (preferably p21). The method is useful for  
 XX producing a recombinant protein in a producer cell line. This is  
 XX particularly useful for maximizing or enhancing the production of e.g.  
 XX therapeutic proteins at an industrial scale

XX Sequence 562 BP; 143 A; 109 C; 163 G; 147 T; 0 U; 0 Other;

Query Match 98.2%; Score 513.8; DB 7; Length 562;  
 Best Local Similarity 99.6%; Pred. No. 2.9e-170;  
 Matches 515; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
 Db 46 CTGCTCCCTGCTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 105  
 Qy 61 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
 Db 106 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 165  
 Qy 121 CTGCTTCGGATGTACGGGCGAGATTCGCGGTATCTGAGGGGATAGGGTGTGTTAGG 180  
 Db 166 CTGCTTCGGATGTACGGGCGAGATTCGCGGTATCTGAGGGGATAGGGTGTGTTAGG 225  
 Qy 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGGATATAGTATTTCGC 240  
 Db 226 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGGATATAGTATTTCGC 285  
 Qy 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Db 286 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 345  
 Qy 301 TAACGATAGTTAGCAACATGCTCTACAGGAGGAAAGACACCGTCATGCCGATGG 360  
 Db 346 TAACGATAGTTAGCAACATGCTCTACAGGAGGAAAGACACCGTCATGCCGATGG 405  
 Qy 361 TGGAGTAAAGTGTGATCGATCGCTTATAGGAGGCAACAGACGGCTCTGACATGGA 420  
 Db 406 TGGAGTAAAGTGTGATCGATCGCTTATAGGAGGCAACAGACGGCTCTGACATGGA 465  
 Qy 421 TTGACGAAACCACTAAATTCGCAATTCGAGATATTGTTATTTAAGTGCCTAGCTCGATA 480  
 Db 466 TTGACGAAACCACTAAATTCGCAATTCGAGATATTGTTATTTAAGTGCCTAGCTCGATA 525  
 Qy 481 CAATAAACGCCATTGACCAATTCACCAATTTGGTGTG 517  
 Db 526 CAATAAACGCCATTGACCAATTCACCAATTTGGTGTG 562

RESULT 6  
 ADD35599  
 ID ADD35599 standard; DNA; 4457 BP.  
 XX  
 AC ADD35599;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Bicistronic eukaryotic expression vector PL178.  
 XX  
 KW Multicistronic eukaryotic expression vector; multiple protein expression;  
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;  
 KW chain terminator; transcription pause site; gene transfer;  
 KW DNA immunisation; gene therapy; PL178; kanamycin resistance gene;  
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;  
 KW hepatitis C virus; HCV IRES; mRSG terminator; cyclic; circular; ds.  
 XX  
 OS Chimeric.  
 OS Synthetic.  
 OS Rous sarcoma virus.  
 OS Oryctolagus cuniculus.  
 OS Hepatitis C virus.  
 OS Escherichia coli.  
 XX  
 XX WO2003031630-A1.  
 XX  
 XX 17-APR-2003.  
 XX  
 XX 10-OCT-2002; 2002WO-IT000646.  
 XX  
 XX 12-OCT-2001; 2001IT-MI002110.  
 XX  
 XX (KERY-) KERYOS SPA.  
 XX  
 XX Pazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;  
 XX MPI; 2003-393446/37.  
 XX  
 XX New multicistronic recombinant plasmid vectors expressing two to our  
 XX genes simultaneously, useful in various biotechnological applications,  
 XX such as gene transfer, gene therapy and in DNA immunization.  
 XX  
 XX Claim 18; SEQ ID NO 2; 52pp; English.  
 XX  
 XX The invention relates to multicistronic eukaryotic expression vectors for  
 XX the expression of at least two proteins of interest which may be  
 XX identical or different. The vectors comprise at least one eukaryotic  
 XX expression cassette having a promoter/enhancer sequence, an intron  
 XX sequence, a cloning site, a viral internal ribosomal entry site (IRES)  
 XX and a chain terminator. The vectors may additionally contain a  
 XX transcription pause site downstream of the chain terminator. The  
 XX invention also encompasses eukaryotic host cells comprising a vector of  
 XX the invention, and the recombinant expression of two or more eukaryotic  
 XX proteins using host cells transfected with a vector of the invention.  
 XX The vectors are useful in various biotechnological applications in which  
 XX the simultaneous expression of two or more genes is necessary, such as  
 XX gene transfer protocols, DNA immunisation, or for the expression of  
 XX different molecules in the same cell. They may also be used in gene  
 XX therapy. The present sequence represents a specifically claimed vector  
 XX designated PL178, which comprises a Rous sarcoma virus (RSV) promoter,  
 XX rabbit beta-globin intron, the hepatitis C virus (HCV) IRES, and a rabbit  
 XX beta-globin gene mRSG terminator as well as a kanamycin resistance gene.  
 XX  
 XX Sequence 4457 BP; 1095 A; 1027 C; 1123 G; 1212 T; 0 U; 0 Other;  
 SQ  
 Query Match 97.3%; Score 508.8; DB 9; Length 4457;  
 Best Local Similarity 99.4%; Pred. No. 5e-168;  
 Matches 521; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTTGTTGAGGTGCTGAGTGTGCGGAGCAAAATTTTAACTACA 60  
 DB 457 CTGCTCCCTGCTGTTGTTGAGGTGCTGAGTGTGCGGAGCAAAATTTTAACTACA 516

QY 61 ACAAGGCAAGGCTTCACCGCAAAATTCGATGAAGAATTCGCTTAGGGTTAGGCTTTTGG 120  
 DB 517 ACAAGGCAAGGCTTCACCGCAAAATTCGATGAAGAATTCGCTTAGGGTTAGGCTTTTGG 576  
 QY 121 CTGCTTCGGGATGTACGGGCGCAGATATTCGCTATCTCAGGGGACTAGGGTGTGTTAGG 180  
 DB 577 CTGCTTCGGGATGTACGGGCGCAGATATTCGCTATCTCAGGGGACTAGGGTGTGTTAGG 636  
 QY 181 CGAAAAGCGGGGCTTCGGTTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC 240  
 DB 637 CGAAAAGCGGGGCTTCGGTTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC 696  
 QY 241 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
 DB 697 TTTTGCATAGGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 756  
 QY 301 TAAAGTGTAGTGTAGCAACATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360  
 DB 757 TAAAGTGTAGTGTAGCAACATGCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTGG 816  
 QY 361 TGAAGTGTAGTGTAGTACGATCGTGCCTTATTAGGAAGCAACAGACGGTCTGACATGA 420  
 DB 817 TGAAGTGTAGTGTAGTACGATCGTGCCTTATTAGGAAGCAACAGACGGTCTGACATGA 876  
 QY 421 TTGACGACCACTAAATTCGCAATTCGACAGAT-ATTGTATTATTAGTGCCTAGCTGAT 479  
 DB 877 TTGACGACCACTAAATTCGCAATTCGACAGAT-ATTGTATTATTAGTGCCTAGCTGAT 936  
 QY 480 ACAATAAACGCCATTGTACCATTCACCAATTTGGTGTGCACCTC 523  
 DB 937 ACAATAAACGCCATTGTACCATTCACCAATTTGGTGTGCACCTC 980  
 RESULT 7  
 ADD35601/c  
 ID ADD35601 standard; DNA; 7334 BP.  
 XX  
 AC ADD35601;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Tetracistronic eukaryotic expression vector PL250.  
 XX  
 KW Multicistronic eukaryotic expression vector; multiple protein expression;  
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;  
 KW chain terminator; transcription pause site; gene transfer;  
 KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;  
 KW cytomagalovirus; CMV promoter/enhancer; CMV intron A;  
 KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;  
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;  
 KW hepatitis C virus; HCV IRES; mRSG terminator; cyclic; circular; ds.  
 XX  
 OS Chimeric.  
 OS Synthetic.  
 OS Human herpesvirus 5.  
 OS Encephalomyocarditis virus.  
 OS Simian virus 40.  
 OS Rous sarcoma virus.  
 OS Oryctolagus cuniculus.  
 OS Hepatitis C virus.  
 OS Escherichia coli.  
 XX  
 XX WO2003031630-A1.  
 XX  
 XX 17-APR-2003.  
 XX  
 XX 10-OCT-2002; 2002WO-IT000646.  
 XX  
 XX 12-OCT-2001; 2001IT-MI002110.  
 XX  
 XX (KERY-) KERYOS SPA.  
 XX  
 XX Pazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;  
 PI

XX WPI; 2003-393446/37.  
 XX New multicistronic recombinant plasmid vectors expressing two to our  
 PT genes simultaneously, useful in various biotechnological applications,  
 PT such as gene transfer, gene therapy and in DNA immunization.  
 XX  
 XX Claim 18; SEQ ID NO 4; 52pp; English.  
 XX  
 CC The invention relates to multicistronic eukaryotic expression vectors for  
 CC the expression of at least two proteins of interest which may be  
 CC identical or different. The vectors comprise at least one eukaryotic  
 CC expression cassette having a promoter/enhancer sequence, an intron  
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)  
 CC and a chain terminator. The vectors may additionally contain a  
 CC transcription pause site downstream of the chain terminator. The  
 CC invention also encompasses eukaryotic host cells comprising a vector of  
 CC the invention, and the recombinant expression of two or more eukaryotic  
 CC proteins using host cells transformed with a vector of the invention.  
 CC The vectors are useful in various biotechnological applications in which  
 CC the simultaneous expression of two or more genes is necessary, such as  
 CC gene transfer protocols, DNA immunisation, or for the expression of  
 CC different molecules in the same cell. They may also be used in gene  
 CC therapy. The present sequence represents a specifically claimed vector  
 CC designated PL250, which comprises a cytomegalovirus (CMV)  
 CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)  
 CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous  
 CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, the hepatitis C  
 CC virus (HCV) IRES, and a rabbit beta-globin gene mRIB terminator as well  
 CC as a kanamycin resistance gene.  
 XX  
 SQ Sequence 7334 BP; 1922 A; 1775 C; 1825 G; 1812 T; 0 U; 0 Other;  
 Query Match 97.3%; Score 508.8; DB 9; Length 7334;  
 Best Local Similarity 99.4%; Pred. No. 6.4e-168;  
 Matches 521; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGGAGTGGCTGAGTGTGCGGAGCAAAATTAAGTACA 60  
 DB 2300 CTGCTCCCTGCTGTGTGGAGTGGCTGAGTGTGCGGAGCAAAATTAAGTACA 2241  
 QY 61 ACAAGGCAAGGCTTACCGCAATTCATGAAGAAATCTGTAGGGTTAGCGTTTGGC 120  
 DB 2240 ACAAGGCAAGGCTTACCGCAATTCATGAAGAAATCTGTAGGGTTAGCGTTTGGC 2181  
 QY 121 CTGCTCGGATGTACGGCCAGATATTCGGTATCTGAGGCACTGAGGTGTGTTAGG 180  
 DB 2180 CTGCTCGGATGTACGGCCAGATATTCGGTATCTGAGGCACTGAGGTGTGTTAGG 2121  
 QY 181 CGAAAGCGGGCTTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
 DB 2120 CGAAAGCGGGCTTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTATTGCG 2061  
 QY 241 TTTTGCATAGGAGGGGAATGTACTCTTAAGCAATCTCTGAGTCTGCAACATGG 300  
 DB 2060 TTTTGCATAGGAGGGGAATGTACTCTTAAGCAATCTCTGAGTCTGCAACATGG 2001  
 QY 301 TAAAGTGTAGTACCAATCCCTTACAAGGAGAAAGACCGTGTGCGCGATTGG 360  
 DB 2000 TAAAGTGTAGTACCAATCCCTTACAAGGAGAAAGACCGTGTGCGCGATTGG 1941  
 QY 361 TGGAGTGTAGTGTACGATCGTCCCTTATTAGGAAGCAACAGCGGCTGTGATGGA 420  
 DB 1940 TGGAGTGTAGTGTACGATCGTCCCTTATTAGGAAGCAACAGCGGCTGTGATGGA 1881  
 QY 421 TTGAGCAACCACTAAATTCGCAATTCGCAAGAT-ATTGTATTAAAGTCCCTACTCGAT 479  
 DB 1880 TTGAGCAACCACTAAATTCGCAATTCGCAAGAT-ATTGTATTAAAGTCCCTACTCGAT 1821  
 QY 480 ACAATAACCCATTTGACATTCACCAATTTGGTGGCCATC 523  
 DB 1820 ACAATAACCCATTTGACATTCACCAATTTGGTGGCCATC 1777

RESULT 8  
 AAQ75974/C  
 ID AAQ75974 standard; cDNA; 4059 BP.  
 XX  
 AC AAQ75974;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 23-AUG-1995 (first entry)  
 XX  
 DE pHLA-B7 expression vector.  
 XX  
 KW expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;  
 KW light beta-2 microglobulin; class I major histocompatibility complex;  
 KW MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.  
 XX  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 misc\_feature 1..354  
 /tag= a  
 /note= "pBR322 backbone contg. bacterial origin of  
 replication"  
 355..1170  
 /tag= b  
 /note= "kanamycin resistance gene open reading frame; the  
 gene is taken from the transposable element Tn903"  
 polyA\_signal  
 /tag= c  
 /note= "SV40 polyA signal sequence"  
 complement(1412..1560)  
 /tag= d  
 /note= "SV40 small t intron"  
 /tag= e  
 /note= "3' untranslated region of HLA-B7 heavy chain  
 mRNA"  
 CDS  
 complement(1795..2880)  
 /tag= f  
 /note= "HLA-B7 open reading frame"  
 complement(2886..3415)  
 /tag= g  
 /note= "Rous sarcoma virus 3' LTR promoter region"  
 3416..4059  
 /tag= h  
 /note= "pBR322 backbone"  
 WO9429469-A2.  
 PD 22-DEC-1994.  
 XX  
 PF 27-MAY-1994; 94WO-US006069.  
 XX  
 PR 07-JUN-1993; 93US-00074344.  
 XX  
 PA (VICA-) VICAL INC.  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Nabel GJ, Nabel EG, Lew D, Marquet M;  
 XX  
 DR WPI; 1995-036494/05.  
 XX  
 PT New vectors for gene therapy, partic for tumours - comprising genetic  
 PT material encoding one or more cistron(s) which express immunogenic or  
 PT therapeutic peptide(s).  
 XX  
 PS Claim 9; Page 42-43; 50pp; English.  
 XX  
 CC This HLA-B7 antigen encoding plasmid was developed to incorporate many  
 CC advantageous features, eg. the kanamycin resistance gene. The  
 CC eradication of two open reading frames encoding portions of SV40 viral  
 CC proteins lowers the risk of tumorigenicity. The vector may also operate  
 CC as a cassette into which cistrons may be inserted and removed at will for  
 CC



```

Db 501 TTGGACGACCACTGAATTCGGATTTCGAGAGATAATTTGTTAAGTGCTAGCTCGAT 560
QY 480 ACAATAAGCCATTGACCAATTCACCACTGGTGTGCACTC 523
Db 561 ACAATAAGCCATTGACCAATTCACCACTGGTGTGCACTC 604

RESULT 10
AAS17704
ID AAS17704 standard; DNA; 4341 BP.
AC AAS17704;
DT 12-MAR-2002 (first entry)
XX Vector pVAC1 encoding a DNA vaccine.
DE Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTL; PCR primer; pVAC1;
KW Clostridium tetani.
OS Homo sapiens.
OS Synthetic.
OS Cauliflower mosaic virus.
XX WO200179510-A1.
XX 25-OCT-2001.
XX 17-APR-2001; 2001WO-GB001719.
XX 17-APR-2000; 2000GB-00009470.
XX (CANC-) CANCER RES VENTURES LTD.
XX Rice J, Stevenson F;
XX WPI; 2002-066370/09.
XX Nucleic acid construct, useful to immunize against various diseases
PT including cancer, expresses the first domain of tetanus toxin FrC fused
PT to a disease peptide antigen to provide a vaccine.
XX Disclosure; Fig 4; 71pp; English.
XX The invention relates to a nucleic acid construct for delivery into
CC living cells in vivo, to induce an immune response to a disease peptide
CC antigen, where the construct directs expression of a fusion protein
CC comprising the peptide antigen and the first domain of FrC. Also included
CC are a nucleic acid vector comprising the above construct, a host cell
CC comprising the above construct or vector and a method of producing a
CC nucleic acid construct for inducing an immune response. The method
CC comprises identifying a nucleic acid sequence encoding a disease peptide
CC antigen comprising epitopes characteristic of the disease, cloning the
CC nucleic acid sequence, introducing the cloned nucleic acid into a vector
CC which allows the antigen to be expressed as a fusion with a first domain
CC FrC from tetanus toxin, and optionally isolating the construct from the
CC vector. The construct or vector is used as a vaccine to induce an immune
CC response, particularly to tumour antigens. The present sequence is vector
CC pVAC1 which encodes a vaccine of the invention
XX Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
Query Match 96.7%; Score 505.6; DB 6; Length 4341;
Best Local Similarity 99.0%; Pred. No. 6.6e-167;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 CTGCTCCCTGCTGTGTGCTGAGGTGCTGAGTAGTGCAGCAAAATTAAGCTACA 60
Db 81 CTGCTCCCTGCTGTGTGCTGAGGTGCTGAGTAGTGCAGCAAAATTAAGCTACA 140
QY 61 ACAAGGCAAGGCTTGACCGACAAATGATGATGAAGAAATCTGCTTAGGGTTAGGGTTTGGC 120

```

```

Db 141 ACAAGGCAAGGCTTGACCGACAAATGATGATGAAGAAATCTGCTTAGGGTTAGGGTTTGGC 200
QY 121 CTGCTCCGAGTAGTACGGGGCAGATATTCGGGTATCTGAGGGACTAGGGTGTCTTTAGG 180
Db 201 CTGCTTCGCGATGTACGGGCGAGATATACGGGTATCTGAGGGGACTAGGGTGTCTTTAGG 260
QY 181 CGAAAAGCGGGGCTTCGGTTGTACGGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240
Db 261 CGAAAAGCGGGGCTTCGGTTGTACGGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 320
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGG 300
Db 321 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGG 380
QY 301 TAACGATGAGTTAGCAACATGCTCTTAAAGGAGAGAAAGACCCGTGCATGCCGATTTGG 360
Db 381 TAACGATGAGTTAGCAACATGCTCTTAAAGGAGAGAAAGACCCGTGCATGCCGATTTGG 440
QY 361 TGGAGGTAAGGTGGTACGATCGTCTTATTAGGAGGCAACAGCGGTCTGCATGGA 420
Db 441 TGGAGGTAAGGTGGTACGATCGTCTTATTAGGAGGCAACAGCGGTCTGCATGGA 500
QY 421 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479
Db 501 TTGACGACCACTAAATTCGCAATTCGAGAGATATTGTATTAAAGTGCCTAGCTCGAT 560
QY 480 ACAATAAGCCATTGACCAATTCACCACTGGTGTGCACTC 523
Db 561 ACAATAAGCCATTGACCAATTCACCACTGGTGTGCACTC 604

RESULT 11
AEN83143
ID AEN83143 standard; DNA; 4341 BP.
XX AEN83143;
AC AEN83143;
DT 10-SEP-2002 (first entry)
XX Plasmid pVAC1 complete sequence.
XX Immune response; plant viral coat protein; pVAC1; cytostatic; virucide;
KW cancer; B cell malignancy; ds.
XX Synthetic.
XX WO200240513-A2.
XX 23-MAY-2002.
XX 20-NOV-2001; 2001WO-GB005142.
XX 20-NOV-2000; 2000GB-00028319.
XX (CANC-) CANCER RES VENTURES LTD.
XX Savelyeva N, Stevenson F;
XX WPI; 2002-500202/53.
XX Nucleic acid construct for delivery into living cells as a vaccine,
PT useful for treating e.g. cancer, directs the expression of a fusion
PT protein comprising an antigen and an adjuvant sequence derived from a
PT plant viral coat protein.
XX Example 3; Fig 7; 84pp; English.
XX The invention relates to a novel nucleic acid construct for inducing an
CC immune response in vivo to an antigen, capable of directing the
CC expression of a fusion protein that comprises an antigen and an adjuvant
CC sequence derived from a plant viral coat protein. The construct of the
CC invention has cytostatic and virucide activity. The nucleic acid

```

CC construct is useful for inducing an immune response in a patient, for  
CC vaccinating a patient against an infectious disease caused by an antigen.  
CC derived from a pathogen e.g. a virus, for treating a cancer patient or a  
CC patient with a predisposition to cancer and for treating a patient having  
CC a B cell malignancy, where the construct is encapsidated, and optionally,  
CC a second nucleic acid sequence encoding a further immunomodulatory  
CC polypeptide is administered to the patient. The construct is also useful  
CC in medical treatment, and in the preparation of a vaccine for treating or  
CC preventing a disease state associated with the antigen. The sequence  
CC shows the complete sequence of vector pVAC1  
XX  
SQ Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;  
Query Match 96.7%; Score 505.6; DB 6; Length 4341;  
Best Local Similarity 99.0%; Pred. No. 6.6e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTGTGGCGAGCAAAATTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTGTGGCGAGCAAAATTAAGCTACA 140  
QY 61 ACAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGCTTAGGGTTAGCGCTTTGGC 120  
Db 141 ACAGGCAAGGCTTGACCGCAATTCGATGAAGATCTGCTTAGGGTTAGCGCTTTGGC 200  
QY 121 CTGCTTCGCGATGTACGGGCGCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTAGG 180  
Db 201 CTGCTTCGCGATGTACGGGCGCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTAGG 260  
QY 181 CGAAAGCGGGCTTCGGT 240  
Db 261 CGAAAGCGGGCTTCGGT 320  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTGTGTGTGTGTGTGTGTGTGTGTGT 300  
Db 321 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTGTGTGTGTGTGTGTGTGTGTGTGT 380  
QY 301 TAACGATGAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGATGCCGATTTGG 360  
Db 381 TAAAGATGAGTGTAGCAATGCCCTTACAAGGAGAGAAAGACCGTGATGCCGATTTGG 440  
QY 361 TGGAGTGTAGGTTGATGATCGTGCCTTATAGGAGGCAACAGCGGTCTGACATGGA 420  
Db 441 TGGAGTGTAGGTTGATGATCGTGCCTTATAGGAGGCAACAGCGGTCTGACATGGA 500  
QY 421 TTGACCAACCACTAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 501 TTGACCAACCACTAATTCGCAATTCGAGATTTTGTATTTAAGTGCCTAGCTCGAT 560  
QY 480 ACAATAAACGCCATTGACCATTCACACATTTGGTGTGCACCTC 523  
Db 561 ACAATAAACGCCATTGACCATTCACACATTTGGTGTGCACCTC 604  
RESULT 12  
AA02998  
ID AA02998 standard; DNA; 5653 BP.  
XX  
AC AA02998;  
XX  
DT 24-MAR-1996 (first entry)  
XX  
DE RSV tar Rev M10 expression plasmid pRSVRevM10.  
XX  
KW Plasmid pRSVRevM10; particle-mediated gene transfer; cyclic;  
KW particle acceleration; HIV virus infection; gene therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..36  
FT /\*tag= a  
FT /\*note= "pBR322 vector sequence"  
FT

FT enhancer 37..610  
FT /\*tag= b  
FT /\*note= "RSV enhancer"  
FT  
FT promoter 611..699  
FT /\*tag= c  
FT /\*label= tar  
FT /\*note= "HIV promoter tat responsive element"  
FT mat\_peptide 700..1129  
FT /\*tag= d  
FT /\*note= "Rev M10 open reading frame"  
FT polyA\_signal 1243  
FT /\*tag= e  
FT /\*note= "cattle somatotropin poly(A) site"  
FT promoter 1993..2300  
FT /\*tag= f  
FT /\*note= "pSVneo promoter"  
FT misc\_feature 2346  
FT /\*tag= g  
FT /\*label= kanamycin\_resistance\_gene  
FT /\*note= "pSV2 neo selectable marker gene"  
FT polyA\_signal 3360  
FT /\*tag= h  
FT /\*note= "pSV2 neo"  
FT misc\_feature 3459..5653  
FT /\*tag= i  
FT /\*note= "plasmid pUC ori/amp sequence"  
XX  
XX WO9529703-A1.  
PN  
XX 09-NOV-1995.  
XX  
XX 01-MAY-1995; 95WO-US005024.  
XX  
XX 29-APR-1994; 94US-00235277.  
XX (NABE/) NABEL G J.  
XX (WOFF/) WOFFENDIN C.  
XX (YANG/) YANG N.  
XX (SHEE/) SHEEHY M J.  
PI Nabel GU, Woffendin C, Yang N, Sheehy MJ;  
XX WPI; 1995-403807/51.  
XX  
XX Particle-mediated gene transfer - in T cells, monocytes, macrophage(s),  
PT dendrites or haematopoietic stem cells, partic. for treating HIV  
PT infection.  
XX  
XX Disclosure; Fig 11a-11e; 96pp; English.  
XX  
XX Expression plasmid pRSVRevM10 contains the Rev M10 HIV protective gene  
CC (a dominant-negative inhibition gene) under the control of the Tar  
CC sequence (HIV promoter -18 to -72), i.e. gene expression is activated by  
CC Tat. The plasmid also contains the kanamycin-resistance selectable  
CC marker gene. The plasmid is used in a particle-mediated gene transfer  
CC process for Rev M10 gene expression in T-cells (preferably), monocytes,  
CC macrophages, haematopoietic stem cells or dendrites. The gold  
CC microparticle acceleration process results in stable incorporation of  
CC foreign genes in the cells. This method is used to treat HIV infection.  
CC Rev M10 transduced cells are resistant to HIV challenge. The method may  
CC be applied to the transfer of other therapeutic genes in a gene therapy  
CC process  
XX  
SQ Sequence 5653 BP; 1328 A; 1428 C; 1478 G; 1419 T; 0 U; 0 Other;  
Query Match 96.7%; Score 505.6; DB 2; Length 5653;  
Best Local Similarity 99.0%; Pred. No. 7.5e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTGTGGCGAGCAAAATTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTGTGGCGAGCAAAATTAAGCTACA 140

QY 61 ACAAGCAAGGCTTACCGACAAATTCATGATGAAGAACTCTGTTAGGTTAGGCTTTTGG 120  
 Db 141 ACAAGCAAGGCTTACCGACAAATTCATGATGAAGAACTCTGTTAGGTTAGGCTTTTGG 200  
 QY 121 CTGCTTCGGATGTACCGGCGCAGATATTCGGCTATCTGAGGGAAGTACGAGGTGTAGG 180  
 Db 201 CTGCTTCGGATGTACCGGCGCAGATATTCGGCTATCTGAGGGAAGTACGAGGTGTAGG 260  
 QY 191 CGAAGAGCGGCTTCGGTGTACCGGCTAGGAGTCCCTCAGGATATAGTGTTCGC 240  
 Db 261 CGAAGAGCGGCTTCGGTGTACCGGCTAGGAGTCCCTCAGGATATAGTGTTCGC 320  
 QY 241 TTTTGCATAGGAGGCGGAAATGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
 Db 321 TTTTGCATAGGAGGCGGAAATGTCTTATGCAATCTCTGTAGTCTTGCACATGG 380  
 QY 301 TAACGATGATTAGCAATGCTTACAGGAGGAGAAAGACCGTCATGCGGATTGG 360  
 Db 381 TAACGATGATTAGCAATGCTTACAGGAGGAGAAAGACCGTCATGCGGATTGG 440  
 QY 361 TGGAGTAAAGTGTACGTCGTCGCTTATTTAGGAGGCAACAGCGGTCTGCATGGA 420  
 Db 441 TGGAGTAAAGTGTACGTCGTCGCTTATTTAGGAGGCAACAGCGGTCTGCATGGA 500  
 QY 421 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 Db 501 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 560  
 QY 480 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 561 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 604

RESULT 13  
 AAT76802  
 ID AAT76802 standard; DNA; 5653 BP.  
 AC AAT76802;  
 XX  
 XX AAT76802;  
 XX  
 DT 18-NOV-1997 (first entry)  
 XX  
 XX RSV tar Rev m10 retroviral vector DNA sequence.  
 XX  
 XX inhibit; Human Immunodeficiency Virus; HIV; gene expression;  
 KW transcription activation region; TAR; negative transdominant mutant;  
 KW Rev M10; mutant; nuclear protein; viral regulatory protein; tat;  
 KW RSV tar Rev M10 plasmid; Rous sarcoma virus; RSV; ds.  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 PH enhancer 37..1129  
 FT /tag= b  
 FT /note= "expression control sequence, contains Rous  
 FT Sarcoma Virus enhancer and Rev M10 gene"  
 FT CDS 700..1129  
 FT /\*tag= a  
 FT /note= "Rev M10 gene"  
 XX  
 XX US650306-A.  
 XX  
 XX 22-JUL-1997.  
 XX  
 XX 07-JUN-1993; 93US-00073836.  
 XX  
 XX 07-JUN-1993; 93US-00073836.  
 XX  
 XX (UNMI ) UNIV MICHIGAN.  
 XX  
 XX Woffendin C, Liu J, Nabel GJ, Yang Z;  
 XX WPI; 1997-384672/35.  
 XX

PT Recombinant nucleic acid for inhibiting HIV gene expression - comprises  
 PT expression control sequence and transcription activation region linked to  
 PT rev negative trans:dominant mutant gene.  
 XX  
 PS Claim 7; Fig 7; 35pp; English.  
 XX  
 CC Recombinant nucleic acid molecules for the improved expression of genes  
 CC which inhibit Human Immunodeficiency Virus (HIV) gene expression are  
 CC claimed, which comprise an expression control sequence and a  
 CC transcription activation region (TAR) sequence, operatively linked to a  
 CC negative transdominant mutant gene (a protective gene), where the  
 CC negative transdominant mutant gene is a mutant of rev. Rev is an 1.8 kDa  
 CC nuclear viral regulatory protein in HIV gene expression which controls  
 CC export of viral RNA from the nucleus to the cytoplasm of infected cells.  
 CC The TAR sequence which is found in the HIV genome controls the regulatory  
 CC activity of the tat protein. The TAR sequence is linked to the protective  
 CC gene, and therefore controls its expression. This sequence is a preferred  
 CC recombinant nucleic acid vector, designated RSV tar Rev M10 plasmid  
 XX  
 SQ Sequence 5653 BP; 1326 A; 1429 C; 1478 G; 1420 T; 0 U; 0 Other;  
 Query Match 96.7%; Score 505.6; DB 2; Length 5653;  
 Best Local Similarity 99.0%; Pred. No. 7.5e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTCTGTTGTTGGAGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGTACA 60  
 Db 81 CTGCTCCCTCTGTTGTTGGAGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGTACA 140  
 QY 61 ACAAGGCAAGGCTTACCGACAAATTCGATGAGTCTGCTGAGTGGCGGAGCAAAATTTAAGTACA 120  
 Db 141 ACAAGGCAAGGCTTACCGACAAATTCGATGAGTCTGCTGAGTGGCGGAGCAAAATTTAAGTACA 200  
 QY 121 CTGCTTCGGATGTACCGGCGCAGATATTCGGCTATCTGAGGGAAGTACGAGGTGTAGG 180  
 Db 201 CTGCTTCGGATGTACCGGCGCAGATATTCGGCTATCTGAGGGAAGTACGAGGTGTAGG 260  
 QY 181 CGAAGAGCGGCTTCGGTGTACCGGCTAGGAGTCCCTCAGGATATAGTGTTCGC 240  
 Db 261 CGAAGAGCGGCTTCGGTGTACCGGCTAGGAGTCCCTCAGGATATAGTGTTCGC 320  
 QY 241 TTTTGCATAGGAGGCGGAAATGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
 Db 321 TTTTGCATAGGAGGCGGAAATGTCTTATGCAATCTCTGTAGTCTTGCACATGG 380  
 QY 301 TAAAGGATGATTAGCAATGCTTACAGGAGGAGAAAGACCGTCATGCGGATTGG 360  
 Db 381 TAAAGGATGATTAGCAATGCTTACAGGAGGAGAAAGACCGTCATGCGGATTGG 440  
 QY 361 TGGAGTAAAGTGTACGTCGTCGCTTATTTAGGAGGCAACAGCGGTCTGCATGGA 420  
 Db 441 TGGAGTAAAGTGTACGTCGTCGCTTATTTAGGAGGCAACAGCGGTCTGCATGGA 500  
 QY 421 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 Db 501 TTGACGAAACCACTAAATTCGCAATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 560  
 QY 480 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 561 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 604  
 RESULT 14  
 AAT76802  
 ID AAT76802 standard; DNA; 5750 BP.  
 XX  
 XX AAT76802;  
 AC AAT76802;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 20-OCT-1993 (first entry)  
 XX  
 XX PRD3D4 construct.  
 XX





CC viruses into cells. It can also be used as for the EGF receptor itself.  
 CC such as in the detection of abnormalities in mammalian cell growth. It is  
 CC also useful for prep. novel receptors for efficient detection of ligands  
 CC and their anti-agonists or agonists. The features table indicates the  
 CC discrepancies between the LD2D3D4 protein sequence given in the  
 CC specification and that which the pRLD2D3D4 DNA sequence given in the  
 CC specification would encode. (Updated on 25-MAR-2003 to correct PF field.)  
 CC  
 XX  
 SQ

Sequence 6207 BP; 1474 A; 1620 C; 1670 G; 1442 T; 0 U; 1 Other;  
 Query Match 96.7%; Score 505.6; DB 2; Length 6207;  
 Best Local Similarity 99.0%; Pred. No. 7.9e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGGAGGTGCTGAGTGTGCGGAGCAGAAATTTAAGCTACA 60  
 DB 81 CTGCTCCCTGCTTGGAGGTGCTGAGTGTGCGGAGCAGAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTGAACGCAATTTGCAATGAAATCTGCTTAGGGTTAGCGTTTGGC 120  
 DB 141 ACAAGGCAAGGCTTGAACGCAATTTGCAATGAAATCTGCTTAGGGTTAGCGTTTGGC 200  
 QY 121 CTGCTTCGCGATGTACGCGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 DB 201 CTGCTTCGCGATGTACGCGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 260  
 QY 181 CGAAAGCGGGCTTCGGTTGTACGCGGTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
 DB 261 CGAAAGCGGGCTTCGGTTGTACGCGGTAGGAGTCCCTCAGGATATAGTATTTCGC 320  
 QY 241 TTTTGTGATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTCGAAATCGG 300  
 DB 321 TTTTGTGATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTCGAAATCGG 380  
 QY 301 TAAAGATGATTAGCAATGCTTCAAGAGAGGAAAGACCGTGCATGCGATTGG 360  
 DB 381 TAAAGATGATTAGCAATGCTTCAAGAGAGGAAAGACCGTGCATGCGATTGG 440  
 QY 361 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGAAAGACCGTGCATGCGATTGG 420  
 DB 441 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGAAAGACCGTGCATGCGATTGG 500  
 QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTCTTACGAT 479  
 DB 501 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTCTTACGAT 560  
 QY 480 ACATTAAGCCATTTGACATTCACCAATTTGGTGTGCACTC 523  
 DB 561 ACATTAAGCCATTTGACATTCACCAATTTGGTGTGCACTC 604

RESULT 16  
 AAQ43812  
 ID AAQ43812 standard; DNA; 6274 BP.  
 AC AAQ43812;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-OCT-1993 (first entry)  
 XX  
 DE pRLD1D2D3.ApA construct.  
 XX  
 KW Epidermal growth factor receptor truncate protein; EGF; growth;  
 KW binding sites; adsorptive agents; mammalian cell growth abnormality;  
 KW detection; reproduction; signal transmission; pRLD1D2D3ApA; ds.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 665..2253  
 FT /\*tag= a  
 FT /codon= 707-708 CG encodes Ile  
 FT /note= "encodes LD1D2D3ApA"

misc\_feature 1939..1941  
 /\*tag= b  
 /note= "codon ARA encodes Ile"  
 XX  
 PN US518090-A.  
 XX  
 PD 08-JUN-1993.  
 XX  
 PF 26-OCT-1990; 90US-00604728.  
 XX  
 PR 12-JUN-1990; 90US-00536896.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Connors RW;  
 XX  
 DR WPI; 1993-196297/24.  
 XX  
 PT P-PSDB; AAR38209.  
 XX  
 PT New epidermal growth factor receptor truncate proteins - which bind  
 PT ligands of EGF receptor without transmitting signal for growth or  
 PT reproduction.  
 XX  
 PS Disclosure; Fig 3; 42pp; English.  
 CC  
 CC The sequence is that of the pRLD1D2D3 construct which encodes the  
 CC epidermal growth factor (EGF) receptor truncate protein LD1D2D3ApA  
 CC having EGF binding sites. The protein binds ligands of the EGF receptor  
 CC without transmitting a signal for the growth and reproduction of a cell.  
 CC It can be used as an adsorptive agent for any moieties that bind the EGF  
 CC receptor as the portal of entry to a cell. It competes with the EGF  
 CC receptor present on the cell surface for the binding of ligands and  
 CC thereby inhibits the action of the ligands or prevents the entry of  
 CC viruses into cells. It can also be used as for the EGF receptor itself,  
 CC such as in the detection of abnormalities in mammalian cell growth. It is  
 CC also useful for prep. novel receptors for efficient detection of ligands  
 CC and their anti-agonists or agonists. The features table indicates the  
 CC discrepancies between the LD1D2D3 protein sequence given in the  
 CC specification and that which the pRLD1D2D3 DNA sequence given in the  
 CC specification would encode. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 0 U; 1 Other;

Query Match 96.7%; Score 505.6; DB 2; Length 6274;  
 Best Local Similarity 99.0%; Pred. No. 8e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGGAGGTGCTGAGTGTGCGGAGCAGAAATTTAAGCTACA 60  
 DB 81 CTGCTCCCTGCTTGGAGGTGCTGAGTGTGCGGAGCAGAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTGAACGCAATTTGCAATGAAATCTGCTTAGGGTTAGCGTTTGGC 120  
 DB 141 ACAAGGCAAGGCTTGAACGCAATTTGCAATGAAATCTGCTTAGGGTTAGCGTTTGGC 200  
 QY 121 CTGCTTCGCGATGTACGCGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 DB 201 CTGCTTCGCGATGTACGCGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 260  
 QY 181 CGAAAGCGGGCTTCGGTTGTACGCGGTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
 DB 261 CGAAAGCGGGCTTCGGTTGTACGCGGTAGGAGTCCCTCAGGATATAGTATTTCGC 320  
 QY 241 TTTTGTGATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTCGAAATCGG 300  
 DB 321 TTTTGTGATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTCGAAATCGG 380  
 QY 301 TAAAGATGATTAGCAATGCTTCAAGAGAGGAAAGACCGTGCATGCGATTGG 360  
 DB 381 TAAAGATGATTAGCAATGCTTCAAGAGAGGAAAGACCGTGCATGCGATTGG 440  
 QY 361 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGAAAGACCGTGCATGCGATTGG 420



XX (AMCY ) AMERICAN CYANAMID CO.  
 PA PA  
 XX Jacobsen JS, Vitek MP;  
 XX WPI; 1997-392937/36.  
 DR P-PSDB; AAW26393.  
 XX Screening for compounds which reduce beta-amyloid protein formation -  
 PT using cells which express a construct encoding a marker and an amyloid  
 PT precursor mutagen derived from APP isoforms.  
 XX  
 PS Disclosure; Fig 7; 84pp; English.  
 XX  
 CC Plasmid pCLL602 (AAW84561), deposited in E. coli as ATCC 69405, codes  
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751  
 CC (see AAW26393), that has a 276-amino acid deletion of the native APP and  
 CC carries Substance P and Met-enkephalin epitope markers placed,  
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid  
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for  
 CC screening for a compound which reduces the formation of beta-amyloid  
 CC protein, determined by measuring the amount of marker in a medium  
 CC containing transfected cells. The method is used to detect compounds  
 CC which inhibit the activity of proteolytic enzymes which cleave APP to  
 CC generate BAP fragments. Such compounds can be used in the treatment of  
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP  
 CC distinguishes the construct from endogenously expressed APP, and  
 CC beneficially increases the resolution of APP-REP fragments resulting from  
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-  
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;  
 Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
 Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60  
 Db 4716 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 4775  
 QY 61 ACAAGGCAAGGCTTGACCGGCAATTCATGAAGAATCTGCTAGGCTTAGGGCTTTTGG 120  
 Db 4776 ACAAGGCAAGGCTTGACCGGCAATTCATGAAGAATCTGCTAGGCTTAGGGCTTTTGG 4835  
 QY 121 CTGCTTCGCGATGTACGGGCGACATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 4836 CTGCTTCGCGATGTACGGGCGACATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 4895  
 QY 181 CGAAAAGCGGGCTTTCGGTGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGG 240  
 Db 4896 CGAAAAGCGGGCTTTCGGTGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGG 4955  
 QY 241 TTTTGTATAGGAGGGGAAATCTAGTCTTATGCAATCTCTGTAGTCTTGTGCAACATGG 300  
 Db 4956 TTTTGTATAGGAGGGGAAATCTAGTCTTATGCAATCTCTGTAGTCTTGTGCAACATGG 5015  
 QY 301 TAACGATGATTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTTGG 360  
 Db 5016 TAACGATGATTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTTGG 5075  
 QY 361 TGGAGTATAGGTGTGATGATGCTTATTTAGGAGGCAACAGACGGGTCTGACATGA 420  
 Db 5076 TGGAGTATAGGTGTGATGATGCTTATTTAGGAGGCAACAGACGGGTCTGACATGA 5135  
 QY 421 TTGAGCAACCACTAAATTCGGCATTTGCAGAGAT-ATTGATTTTAAAGTCCCTAGCTCGAT 479  
 Db 5136 TTGAGCAACCACTAAATTCGGCATTTGCAGAGATTAATTTTAAAGTCCCTAGCTCGAT 5195  
 QY 480 ACATAAGCGCATTTGACCATTCACCATTTGGTGTGACCTC 523  
 Db 5196 ACATAAGCGCATTTGACCATTCACCATTTGGTGTGACCTC 5239

RESULT 19  
 AAT87083  
 ID AAT87083 standard; CDNA; 8591 BP.  
 XX  
 AC AAT87083;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 06-JAN-1998 (first entry)  
 XX  
 DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.  
 XX  
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;  
 KW mutagen; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;  
 KW cyclic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 2393..3871  
 FT /\*tag= a  
 FT  
 FT US5656477-A.  
 FN  
 XX 12-AUG-1997.  
 PD  
 XX 20-SEP-1993; 93US-00123659.  
 PF  
 XX 01-MAY-1992; 92US-00877675.  
 PR  
 XX (AMCY ) AMERICAN CYANAMID CO.  
 PA  
 XX Jacobsen JS, Vitek MP;  
 PI WPI; 1997-414594/38.  
 DR P-PSDB; AAW26509.  
 XX  
 PT Nucleic acid encoding amyloid precursor mutagen(s) - comprising reporter  
 PT gene and coding sequence, for identifying compounds which modify the  
 PT activity of proteolytic enzymes which cleave APP.  
 PS  
 PS Disclosure; Fig 7; 84pp; English.  
 XX  
 CC Plasmid pCLL602 (AAT87083), deposited in E. coli as ATCC 69405, codes  
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751  
 CC (see AAW26509), that has a 276-amino acid deletion of the native APP and  
 CC carries Substance P and Met-enkephalin epitope markers placed,  
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid  
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for  
 CC screening for a compound which reduces the formation of beta-amyloid  
 CC protein, determined by measuring the amount of marker in a medium  
 CC containing transfected cells. The method is used to detect compounds  
 CC which inhibit the activity of proteolytic enzymes which cleave APP to  
 CC generate BAP fragments. Such compounds can be used in the treatment of  
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP  
 CC distinguishes the construct from endogenously expressed APP, and  
 CC beneficially increases the resolution of APP-REP fragments resulting from  
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-  
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;  
 Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
 Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 60  
 Db 4716 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGAGCAAAATTAAGCTACA 4775  
 QY 61 ACAAGGCAAGGCTTGACCGGCAATTCATGAAGAATCTGCTAGGCTTAGGGCTTTTGG 120  
 Db 4776 ACAAGGCAAGGCTTGACCGGCAATTCATGAAGAATCTGCTAGGCTTAGGGCTTTTGG 4835  
 QY 121 CTGCTTCGCGATGTACGGGCGACATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 4836 CTGCTTCGCGATGTACGGGCGACATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 4895  
 QY 181 CGAAAAGCGGGCTTTCGGTGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGG 240  
 Db 4896 CGAAAAGCGGGCTTTCGGTGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGG 4955  
 QY 241 TTTTGTATAGGAGGGGAAATCTAGTCTTATGCAATCTCTGTAGTCTTGTGCAACATGG 300  
 Db 4956 TTTTGTATAGGAGGGGAAATCTAGTCTTATGCAATCTCTGTAGTCTTGTGCAACATGG 5015  
 QY 301 TAACGATGATTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTTGG 360  
 Db 5016 TAACGATGATTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTTGG 5075  
 QY 361 TGGAGTATAGGTGTGATGATGCTTATTTAGGAGGCAACAGACGGGTCTGACATGA 420  
 Db 5076 TGGAGTATAGGTGTGATGATGCTTATTTAGGAGGCAACAGACGGGTCTGACATGA 5135  
 QY 421 TTGAGCAACCACTAAATTCGGCATTTGCAGAGAT-ATTGATTTTAAAGTCCCTAGCTCGAT 479  
 Db 5136 TTGAGCAACCACTAAATTCGGCATTTGCAGAGATTAATTTTAAAGTCCCTAGCTCGAT 5195  
 QY 480 ACATAAGCGCATTTGACCATTCACCATTTGGTGTGACCTC 523  
 Db 5196 ACATAAGCGCATTTGACCATTCACCATTTGGTGTGACCTC 5239

Db 4776 ACAGGCGAGGCTTGACCGACATTCGATGAGATCTGCTAGGGTTAGGGCTTTTCGG 4835  
QY 121 CTGCTTCGCGATGACGGGCGAGATATTTCGGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGACGGGCGAGATATTTCGGCTATCTGAGGGGACTAGGGTGTGTTAGG 4895  
QY 181 CGAAAGCGGGCTTGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTATGTTTCG 240  
Db 4896 CGAAAGCGGGCTTGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTATGTTTCG 4955  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTCGACATGG 300  
Db 4956 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTCGACATGG 5015  
QY 301 TACGATGATGATGACATGCTTACAGGAGAGAAAGCAGCGTGCATGCCATGG 360  
Db 5016 TACGATGATGATGACATGCTTACAGGAGAGAAAGCAGCGTGCATGCCATGG 5075  
QY 361 TGAAGTAAGTGTGACGATGCTTATTAGGAGGCAACAGACGGGCTGACATGGA 420  
Db 5076 TGAAGTAAGTGTGACGATGCTTATTAGGAGGCAACAGACGGGCTGACATGGA 5135  
QY 421 TTGGACGACCACTAATTCGGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 5136 TTGGACGACCACTAATTCGGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 5195  
QY 480 ACAATAAACGCCATTTCGACATTCACCAATTCGACATTCGACATTCGACATTC 523  
Db 5196 ACAATAAACGCCATTTCGACATTCACCAATTCGACATTCGACATTCGACATTC 5239

RESULT 20

AAT87084  
ID AAT87084 standard; cDNA; 8591 BP.  
XX  
AC AAT87084;  
XX  
XX  
DT 25-MAR-2003 (revised)  
DT 06-JAN-1998 (first entry)  
XX  
XX Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.  
XX  
XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;  
XX mutain; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;  
XX cyclic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.

PH Key Location/Qualifiers  
FT CDS 2393..3856  
FT /\*tag= a  
XX  
XX US5656477-A.  
XX  
XX 12-AUG-1997.  
XX  
XX 20-SEP-1993; 93US-00123659.  
XX  
XX 01-MAY-1992; 92US-00877675.  
XX  
XX (AMCY ) AMERICAN CYANAMID CO.  
XX  
XX Jacobsen JS, Vitek MP;  
PI  
XX  
XX WPI; 1997-414594/38.  
XX P-PSDB; AAW26510.  
XX  
XX Nucleic acid encoding amyloid precursor mutin(s) - comprising reporter  
PT gene and coding sequence, for identifying compounds which modify the  
PT activity of proteolytic enzymes which cleave APP.

XX  
PS  
XX  
CC Plasmid pCLL621 (AAT87084), deposited in E. coli as ATCC 69406, codes  
CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751  
CC (see AAW26510), that has a 276-amino acid deletion of the native APP and  
CC carries a substance P epitope marker on the N-terminal side of the beta-  
CC amyloid protein (BAP) domain. APP-REP 751 can be used in a claimed method  
CC for screening for a compound which reduces the formation of beta-amyloid  
CC protein, determined by measuring the amount of marker in a medium  
CC containing transfected cells. The method is used to detect compounds  
CC which inhibit the activity of proteolytic enzymes which cleave APP to  
CC generate BAP fragments. Such compounds can be used in the treatment of  
CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP  
CC distinguishes the construct from endogenously expressed APP, and  
CC beneficially increases the resolution of APP-REP fragments resulting from  
CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-  
CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;  
Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTTCCTGCTTGTGTGTTGGAGTGGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 4716 CTGCTTCCTGCTTGTGTGTTGGAGTGGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 4775  
QY 61 ACAGGCGAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGGTTAGGCTTTTCGG 120  
Db 4776 ACAGGCGAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGGTTAGGCTTTTCGG 4835  
QY 121 CTGCTTCGCGATGTACGGGCGCAGATATTTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGTACGGGCGCAGATATTTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 4895  
QY 181 CGAAAGCGGGCTTGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTATGTTTCG 240  
Db 4896 CGAAAGCGGGCTTGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTATGTTTCG 4955  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTCGACATGG 300  
Db 4956 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTCGACATGG 5015  
QY 301 TACGATGATGATGACATGCTTACAGGAGAGAAAGCAGCGTGCATGCCATGG 360  
Db 5016 TACGATGATGATGACATGCTTACAGGAGAGAAAGCAGCGTGCATGCCATGG 5075  
QY 361 TGAAGTAAGTGTGACGATGCTTATTAGGAGGCAACAGACGGGCTGACATGGA 420  
Db 5076 TGAAGTAAGTGTGACGATGCTTATTAGGAGGCAACAGACGGGCTGACATGGA 5135  
QY 421 TTGGACGACCACTAATTCGGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479  
Db 5136 TTGGACGACCACTAATTCGGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 5195  
QY 480 ACAATAAACGCCATTTCGACATTCACCAATTCGACATTCGACATTCGACATTC 523  
Db 5196 ACAATAAACGCCATTTCGACATTCACCAATTCGACATTCGACATTCGACATTC 5239  
RESULT 21  
AAV04866  
ID AAV04866 standard; DNA; 8591 BP.  
XX  
AC AAV04866;  
XX  
XX 01-MAY-1998 (first entry)  
XX  
XX cDNA encoding amyloid precursor protein mutant APP-APP 751.  
XX Beta-amyloid peptide; BAP; extracellular BAP plaque;  
XX

cerebrovascular deposit; Alzheimers disease; Downs syndrome;  
amyloid precursor protein; App; secretase; BAP aggregation;  
abnormal proteolytic cleavage; ds.

XX Synthetic.

OS Homo sapiens.

XX			
FH	Key	Location/Qualifiers	
FT	CDS	2393. .3856	
FT		/*taq= a	

XX  
PN US5703209-A.XX  
PD 30-DEC-1997.

XX  
PF 05-JUN-1995; 95US-00464248.

XX  
PR 01-MAY-1992: 92US-00877675.

20-SEP-1993; 93US-00123659. PR

XX  
PA (AMCY ) AMERICAN CYANAMID CO.

XX  
PI Jacobsen JS, Vitek MP;

XX  
DR WPI; 1998-076482/07.

DR P-PSDB; AAW42979.

XX Amyloid precursor protein fusion polypeptides - comprising APP fragment  
PT and marker, useful for research and drug screening.

PS Disclosure; Fig 8A-Q; 84pp; English.

XX CC The present sequence encodes an amyloid precursor protein (APP), which  
CC has a deletion of 276 amino acids to within 15 amino acids of the beta-  
CC amyloid peptide (BAP) domain. The protein also contains the Abnormal  
CC accumulation of extracellular BAP in plaques and cerebrovascular deposits  
CC is characteristic in brains of individuals suffering from Alzheimer's  
CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating  
CC protein which is derived from a larger amyloid precursor protein (APP).  
CC APP is expressed as an integral membrane protein, and is cleaved by  
CC secretase, between BAP 161lys and 171leu. Cleavage at this site precludes  
CC amyloidogenesis and results in the release of the amino-terminal APP  
CC fragment. three major isoforms of APP exist: APP-695, APP-751 and APP-  
CC 770. These isoforms are derived by alternative splicing. APP-RPP 751 is  
CC constructed by ligating restriction fragments representing N- and C-  
CC terminal APP-751 cDNA and substrate p reporter epitope sequences. APP  
CC can be used as a substrate for studying abnormal proteolytic cleavage  
CC which results in the release of BAP, and also to screen for drugs that  
CC will inhibit such cleavage

Sequence 8591 BP: 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match	96.7%;	Score 505.6;	DB 2;	Length 8591;
Best Local Similarity	99.0%;	Pred. No. 9.4e-167;		
Wobler 510.	Conservative	0.	Mismatches 4;	Indels 1;
				Gaps 1;

[illegible][illegible]

DB 4776 ACNAGGCAAGCGTTGACCGACAATGCAAGAGAAATGCTCTTAGGGTAGGCGGCTTTTGGG 4905

QY 121 CTCGCTCCGGATGTACGGGCGAGATAATCCGCTACTCTGAGGGGACTAGGGTGTGTTTAGG 180

4836 CTGCTTCGCGTGATACGGGCCAGATATACCGCTATCTGAGGGACATAGGGGAGGCTGTTAGG 4893  
Db  
181 CGAAGAGCGGSCCTTCGTTGTATCGCGTTTAGAGCTCCCTCAGGATATAGTAGTTCCG 240  
Qy

Accession	Gene	Accession	Gene
DB	CGAARAAGCGGGGCTTCGGTTGTACCGGTTAGGAGTCCCGCTCAGGATATAGTAGTTTCGC	241	TTTTTTCGATAGGAGCGGGGAAATGAGTCTTTATGCAATACTCTTGTAGTCTTGCACAATGG
	4896		300

Db	4956	TTTTGCATATGGGAGGGGAAATGTAGCTTTATGCAATACACTTTGTAGTCTTGCACAATGG	5015
Qy	301	TAAACATGAGTTTAGCAACATCGCTTACAGGAGAGAAAAAGCACCGTGATGCGATGCGGATTTGG	360
Db	5016	TAAOCATGAGTTTAGCAACATCGCTTTACAGGAGAGAAAAAGCACCGTGATGCGGATTTGG	5075
Qy	361	TGGAAGTAAGAGTGGTACGATCGTCGCTTTATTAGGAAGCGCAACAGACGGGTCTGCATGGA	420
Db	5076	TGGAAGTAAGAGTGGTACGATCGTCGCTTTATTAGGAAGCGCAACAGACGAGTCTGCATGGA	5135
Qy	421	TTTGGACGACCACTAAATTCGGATTCGACAGAT-ATTGTATTAAAGTGCTAGCTCGAT	479
Db	5136	TTTGGACGACCACTGAATTCGGATTCGACAGATATTGTATTAAAGTGCTAGCTCGAT	5195
Qy	480	ACAAATAACGCCATTGTACCACTTACCAACATTGGTGTGCACCTC	523
Db	5196	ATGATTAACGCTATTGTACCACTTACCAACATTGGTGTGCACCTC	5239

RESULT 22

AAV04865

AAV04865

AC  
XX  
AAV04865;

DT 01-MAY-1998 (first entry)  
XX  
DE cDNA encoding amyloid precursor protein mutant APP-APP 751.

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;  
 KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;  
 KW amyloid precursor protein; APP; secrete; BAP aggregation;  
 KW abnormal proteolytic cleavage; ds.

XX  
XX  
OS Homo sapiens.

XX	Key	Location/Qualifiers
FH	Key	2393. .3871
FT	CDS	/#tag= a
FT		

FX  
XX  
DN  
UG5703209-A

FN XX DD  
035703203-A.  
30-DEC-1997

FD 30-DEC-1997;  
XX  
DE 05-JUN-1995;  
95US-00464248

03-00A-1000;  
XX  
01-MAY-1992;  
92US-00877675;  
PR

PR 20-SEP-1993; 93US-00123659.  
XX

PA (AMCY ) AMERICAN CYANAMID CO.  
XX

PI Jacobsen JS, Vittek MP;  
XX

DR WPI; 1998-076482/07.  
DR P-PSDB; AAW42978.

XX  
pT Amyloid precursor

XX  
pg  
pt and marker, useful for research and drug screening.  
XX  
pg  
Discoloration: Fig 7A-O. 84pp. English.

FS disclosed; 119 (11 2) 0.12) 203-223  
XX  
CC The present sentence encodes an amyli

has a deletion of 276 amino acids to within 15 amino acids of the beta-amyloid peptide (BAP) domain. The protein also contains the Met-enkephalin reporter epitope at the carboxy terminus. Abnormal accumulation of extracellular BAP in plaques and cerebrovascular deposits is characteristic in brains of individuals suffering from Alzheimer's disease and Downs syndrome. BAP is a poorly soluble, self-aggregating protein which is derived from a larger amyloid precursor protein (APP). APP is expressed as an integral membrane protein, and is cleaved by secretase, between BAP 161yfs and 171yfs. Cleavage at this site precludes amyloidogenesis and results in the release of the amino-terminal APP

CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-770. These isoforms are derived by alternative splicing. APP-REP 751 is constructed by ligating restriction fragments representing N- and C-terminal APP-751 cDNA and substrate P reporter epitope sequences. APP can be used as a substrate for studying abnormal proteolytic cleavage which results in the release of BAP, and also to screen for drugs that will inhibit such cleavage

XX SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGCTGCTGAGGTGCTGAGTAGTGGCGAGCAAAATTTAGCTACA 60  
DB 4716 CTGCTCCCTGCTGCTGCTGAGGTGCTGAGTAGTGGCGAGCAAAATTTAGCTACA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTTCG 120  
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTTCG 4835

QY 121 CTGCTCCGATGTACGGCCAGATATTCGCGTATCTAGAGGCACTAGGTTGTTAGG 180  
DB 4836 CTGCTCCGATGTACGGCCAGATATTCGCGTATCTAGAGGCACTAGGTTGTTAGG 4895

QY 181 CGAAAAGCGGGCTTCGGTTGACGCGTATACGCGTATCTGAGGCGGACTAGGTTGTTAGG 240  
DB 4896 CGAAAAGCGGGCTTCGGTTGACGCGTATACGCGTATCTGAGGCGGACTAGGTTGTTAGG 4955

QY 241 TTTTTCATAGGAGGGGAAATGAGTCTTATGCAATCTCTGTTAGTTGCAACATGG 300  
DB 4956 TTTTTCATAGGAGGGGAAATGAGTCTTATGCAATCTCTGTTAGTTGCAACATGG 5015

QY 301 TTAAGATGAGTTAGCAACATGCTTACAGGAGAGAAAGCAAGCGTGCATGCCGATTGG 360  
DB 5016 TTAAGATGAGTTAGCAACATGCTTACAGGAGAGAAAGCAAGCGTGCATGCCGATTGG 5075

QY 361 TGGAGTAAAGTGTACGATCGTCTTATAGAGGCAACAGACGGGTCTGCATGGA 420  
DB 5076 TGGAGTAAAGTGTACGATCGTCTTATAGAGGCAACAGACGGGTCTGCATGGA 5135

QY 421 TTGGACGAACCACTAAATTCGCGATTCAGAGAT-ATTGTTATTAAGTCCCTAGCTCGAT 479  
DB 5136 TTGGACGAACCACTAAATTCGCGATTCAGAGAT-ATTGTTATTAAGTCCCTAGCTCGAT 5195

QY 480 ACAATAAGCCCATTTGACCATTCACCAATTTGGTGTGCACCTC 523  
DB 5196 ACAATAAGCCCATTTGACCATTCACCAATTTGGTGTGCACCTC 5239

RESULT 23  
AAV05850 standard; cDNA; 8591 BP.  
AC AAV05850;  
XX AAV05850;  
DT 01-JUN-1998 (first entry)  
XX APP-REP 751 gene from pCLL621.  
DE  
XX Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;  
KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;  
KW Alzheimer's disease; cleavage; cyclic; circular; ds.  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH 2393..3856  
FT CDS /tag= a  
FT /product= "APP\_REP\_751"  
XX

PN US5693478-A.  
XX  
PD 02-DEC-1997.  
XX  
XX 05-JUN-1995; 95US-00464247.  
XX  
XX 01-MAY-1992; 92US-00877675.  
XX  
XX 20-SEP-1993; 93US-00123659.  
XX  
XX (AWCY ) AMERICAN CYANAMID CO.  
XX  
XX Jacobsen JS, Vitek MP;  
PI  
XX WPI; 1998-031744/03.  
DR  
XX P-PSDB; AAW44745.  
XX  
XX Amyloid precursor mutin reporter molecule assay containing antibody  
PT recognised marker - used to study pathways associated with Alzheimer's  
PT disease.  
XX  
XX Disclosure; Fig 8; 84pp; English.  
XX  
XX This is the nucleotide sequence encoding a novel amyloid precursor  
CC protein (APP) designated APP-REP 751, contained in construct pCLL621. The  
CC sequence encodes a mutant version of the APP 751 isoform of human APP  
CC which contains a deletion of 276 amino acids from the central region. The  
CC deleted region is replaced by a substrate P reporter epitope sequence  
CC (RPKQQFFGLM). In contrast to the APP-REP 751 encoded by the construct  
CC pCLL602 (AAV5849), this sequence does not contain a Met-enkephalin  
CC reporter epitope (YGGFM) fused at the C-terminus of the coding sequence.  
CC The shorter protein is generated for ease of detection based on size  
CC difference with the wild type APP protein and also by detection of the  
CC reporter epitopes. The mutant protein can be used in a method to study  
CC secretase and beta-amyloid protein (BAP)-generating pathways associated  
CC with Alzheimer's disease by studying proteolytic cleavage of the reporter  
CC polypeptides  
XX  
XX Sequence 8591 BP; 2225 A; 2038 C; 2248 G; 2080 T; 0 U; 0 Other;  
SQ

Query Match 96.7%; Score 505.6; DB 2; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 9.4e-167;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGCTGCTGAGGTGCTGAGTAGTGGCGAGCAAAATTTAGCTACA 60  
DB 4716 CTGCTCCCTGCTGCTGCTGAGGTGCTGAGTAGTGGCGAGCAAAATTTAGCTACA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTTCG 120  
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTTCG 4835

QY 121 CTGCTCCGATGTACGGCCAGATATTCGCGTATCTAGAGGCACTAGGTTGTTAGG 180  
DB 4836 CTGCTCCGATGTACGGCCAGATATTCGCGTATCTAGAGGCACTAGGTTGTTAGG 4895

QY 181 CGAAAAGCGGGCTTCGGTTGACGCGTATACGCGTATCTGAGGCGGACTAGGTTGTTAGG 240  
DB 4896 CGAAAAGCGGGCTTCGGTTGACGCGTATACGCGTATCTGAGGCGGACTAGGTTGTTAGG 4955

QY 241 TTTTTCATAGGAGGGGAAATGAGTCTTATGCAATCTCTGTTAGTTGCAACATGG 300  
DB 4956 TTTTTCATAGGAGGGGAAATGAGTCTTATGCAATCTCTGTTAGTTGCAACATGG 5015

QY 301 TTAAGATGAGTTAGCAACATGCTTACAGGAGAGAAAGCAAGCGTGCATGCCGATTGG 360  
DB 5016 TTAAGATGAGTTAGCAACATGCTTACAGGAGAGAAAGCAAGCGTGCATGCCGATTGG 5075

QY 361 TGGAGTAAAGTGTACGATCGTCTTATAGAGGCAACAGACGGGTCTGCATGGA 420  
DB 5076 TGGAGTAAAGTGTACGATCGTCTTATAGAGGCAACAGACGGGTCTGCATGGA 5135

QY 421 TTGGACGAACCACTAAATTCGCGATTCAGAGAT-ATTGTTATTAAGTCCCTAGCTCGAT 479  
DB 5136 TTGGACGAACCACTAAATTCGCGATTCAGAGAT-ATTGTTATTAAGTCCCTAGCTCGAT 479

Db 5136 TTGGACGACCACTGAAATTCGGATTGCGAGATTAATGTTAATTAAGTGGCTAGCTCGAT 5195

QY 480 ACATTAAGCGCATTTGACCATTCACGACATTCGTTGGTGGACCTC 523

Db 5196 ACAATAAGCGCATTTGACCATTCACGACATTCGTTGGTGGACCTC 5239

RESULT 24

AAV05849

ID AAV05849 standard; cDNA; 8591 BP.

XX

AC AAV05849;

XX

DT 01-JUN-1998 (first entry)

XX

DE APP-REP 751 gene from pCLL602.

XX

KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;

KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;

KW Alzheimer's disease; cleavage; cyclic; circular; ds.

XX

OS Homo sapiens.

OS Synthetic.

XX

FE Key Location/Qualifiers

FT CDS 2393..3871

FT /\*tag= a

FT /product= "APP-REP\_751"

XX

PN US5693478-A.

XX

PD 02-DEC-1997.

XX

PF 05-JUN-1995; 95US-00454247.

XX

PR 01-MAY-1992; 92US-00877675.

PR 20-SEP-1993; 93US-00123659.

XX

PA (AMCY ) AMERICAN CYANAMID CO.

XX

PI Jacobsen JS, Vitek WP;

XX

DR WPI; 1998-031744/03.

DR P-PSDB; AAW44744.

XX

FT Amyloid precursor muten reporter molecule assay containing antibody

FT recognised marker - used to study pathways associated with Alzheimer's

PT disease.

XX

PS Disclosure; Fig 7; 84pp; English.

XX

CC This is the nucleotide sequence encoding a novel amyloid precursor

CC protein (APP) designated APP-REP 751, contained in construct pCLL602. The

CC sequence encodes a mutant version of the APP 751 isoform of human APP

CC which contains a deletion of 276 amino acids from the central region. The

CC deleted region is replaced by a substrate P reporter epitope sequence

CC (RPKQQPFGIM) and a Met-enkephalin reporter epitope (YGGFW) is fused at

CC the C-terminus. The shorter protein is generated for ease of detection

CC based on size difference with the wild type APP protein and also by

CC detection of the reporter epitopes. The mutant protein can be used in a

CC method to study secretase and beta-amyloid protein (BAP)-generating

CC pathways associated with Alzheimer's disease by studying proteolytic

CC cleavage of the reporter polypeptides

XX

SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 96.7%; Score 505.6; DB 2; Length 8591;

Best Local Similarity 99.0%; Pred. No. 9.4e-167;

Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGTTGTGTGTTGGAGTGGCTGAGTGGCGAGCAAAATTTAAGCTACA 60

Db 4716 CTGCTCCCTGTTGTGTGTTGGAGTGGCTGAGTGGCGAGCAAAATTTAAGCTACA 4775

QY 61 ACAAGGCAAGGCTTGACCGCAAAATTCATGAAGAATCTCTTAGGGTTAGGCGTTTGGC 120

Db 4776 ACAAGGCAAGGCTTGACCGCAAAATTCATGAAGAATCTCTTAGGGTTAGGCGTTTGGC 4835

QY 121 CTGCTTCGCGATGTAAGGCGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTTAGG 180

Db 4836 CTGCTTCGCGATGTAAGGCGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTTAGG 4895

QY 181 CGAAAAGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240

Db 4896 CGAAAAGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 4955

QY 241 TTTTGCATAGGAGGGGGGAATGTAGTCTTTATGCAATCTCTTGTAGTCTTGCACATGG 300

Db 4956 TTTTGCATAGGAGGGGGGAATGTAGTCTTTATGCAATCTCTTGTAGTCTTGCACATGG 5015

QY 301 TAAACGATGATTAAGCAACATCGCTTCAAGGAGAGAAAAGCACCGTGCATGCCGATGG 360

Db 5016 TAAACGATGATTAAGCAACATCGCTTCAAGGAGAGAAAAGCACCGTGCATGCCGATGG 5075

QY 361 TGGAAAGTAAGGTGTACGATCGTCTTATTAGGAGGCAACAGACGGTCTGCACATGGA 420

Db 5076 TGGAAAGTAAGGTGTACGATCGTCTTATTAGGAGGCAACAGACGGTCTGCACATGGA 5135

QY 421 TTGGACGACCACTAAATTCGGCATTTGCGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479

Db 5136 TTGGACGACCACTAAATTCGGCATTTGCGAGATATTGTATTTAAGTCCCTAGCTCGAT 5195

QY 480 ACAATAAACGCCATTTTGACCATTCACCAATTTGGTGTGCACCTC 523

Db 5196 ACAATAAACGCCATTTTGACCATTCACCAATTTGGTGTGCACCTC 5239

RESULT 25

AAT62602

ID AAT62602 standard; DNA; 7223 BP.

XX

AC AAT62602;

XX

DT 25-MAR-2003 (revised)

DT 12-MAY-1997 (first entry)

XX

DE Luciferase expression vector, prsvLuc.

XX

KW NLS; 126-132; SV40 Large T antigen; nuclear location signal; transport;

KW inducible repressor; vector; expression; exogenous; eukaryotic cell;

KW transgenic animal; model; human disease; ss.

XX

OS Synthetic.

XX

PN US5589392-A.

XX

PD 31-DEC-1996.

XX

PF 29-NOV-1993; 93US-00158718.

XX

PR 14-JAN-1991; 91US-00640983.

XX

PA (STRA-) STRATAGENE.

XX

PI Short JM;

XX

DR WPI; 1997-107141/10.

XX

PT Nucleic acid construct for gene expression - comprising DNA sequences

PT encoding nuclear transport signal peptide and inducible repressor.

XX

PS Example 2; Col 43-50; 43pp; English.

XX

CC DNA constructs encoding a nuclear transport signal operatively linked to

CC a DNA sequence encoding an inducible repressor are useful as vectors for

CC expression of exogenous genes in eukaryotic cells in vitro and in vivo,



CC e.g. for production of transgenic animals as models for human diseases.  
CC The present sequence is that of a luciferase reporter expression vector,  
CC pRSLuc. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 7223 BP; 1880 A; 1730 C; 1864 G; 1745 T; 0 U; 4 Other;  
  
Query Match 96.5%; Score 504.6; DB 2; Length 7223;  
Best Local Similarity 99.0%; Pred. No. 1.9e-166;  
Matches 518; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
  
QY 1 CTGCTCCCTGCTTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTAAGTACA 60  
Db 2106 CTGCTCCCTGCTTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTAAGTACA 2165  
  
QY 61 ACAAGCAAGGTTGACCGCAATTCGATGAGAAATCTGCTTAGGTTAGCGGTTTGG 120  
Db 2166 ACAAGCAAGGTTGACCGCAATTCGATGAGAAATCTGCTTAGGTTAGCGGTTTGG 2225  
  
QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180  
Db 2226 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 2285  
  
QY 181 CGAAAGCGGGCTTCGCTGTGTACGGGTTAGGAGTCCCTCAGATATAGTATTCGC 240  
Db 2286 CGAAAGCGGGCTTCGCTGTGTACGGGTTAGGAGTCCCTCAGATATAGTATTCGC 2345  
  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
Db 2346 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 2405  
  
QY 301 TAAACGATGCTTACCAATCCCTTAAAGGAGAGAAAGACCGTGCATGCCGATGG 360  
Db 2406 TAAACGATGCTTACCAATCCCTTAAAGGAGAGAAAGACCGTGCATGCCGATGG 2465  
  
QY 361 TGAAGTAAGTGGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGTCTGACATGA 420  
Db 2466 TGAAGTAAGTGGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGTCTGACATGA 2525  
  
QY 421 TTGACCAACCACTAATTCGCAATTCGAGAGAT-ATTGTATTAAAGTCCCTAGCTCGAT 479  
Db 2526 TTGACCAACCACTAATTCGCAATTCGAGAGATATTGTATTAAAGTCCCTAGCTCGAT 2585  
  
QY 480 ACAATAAACGCCATTGACCAATTCACCAATTCGATGTCACCT 522  
Db 2586 ACAATAAACGCCATTGACCAATTCACCAATTCGATGTCACCT 2628  
  
RESULT 26  
AAA53869  
ID AAA53869 standard; DNA; 6838 BP.  
XX  
XX AC AAA53869;  
XX DT 03-JAN-2001 (first entry)  
XX DE Expression vector pRIG-1.  
XX KW Vector; endogenous gene; activation; over-expression; erythropoietin;  
KW growth hormone; drug discovery; granulocyte colony stimulating factor;  
KW ds.  
XX OS Synthetic.  
XX FN WO200049162-A2.  
XX PD 24-AUG-2000.  
XX PF 22-FEB-2000; 2000WO-US004429.  
XX PR 19-FEB-1999; 99US-00253022.  
XX PR 08-MAR-1999; 99US-00263814.  
XX PR 26-MAR-1999; 99US-00276820.  
XX

PA (ATHE-) ATHERSYS INC.  
XX  
PI Harrington J, Sherr B, Rundlett S;  
XX  
XX WPI; 2000-549276/50.  
XX  
XX Non-targeted activation of endogenous genes, e.g. for the production of  
XX erythropoietin, growth hormone or granulocyte-colony stimulating factor  
XX proteins and for drug discovery.  
XX  
XX Example 1; Fig 14; 240pp; English.  
XX  
XX New methods, vectors and cells are described for non-targeted activation  
XX and over-expression of endogenous genes. The vector constructs comprise  
XX transcriptional regulatory sequences (TRS) and unpaired splice donor  
XX sequences (USDS), preferably the vectors comprise (in sequential order) a  
XX TRS, an USDS, a rare cutting restriction site (RCS) and a linearization  
XX site (LS) with a second TRS linked to a selectable marker (SM) lacking a  
XX polyadenylation signal. The methods, vectors and cells comprising the  
XX vectors may be used for the non-targeted activation and over-expression  
XX of endogenous genes, e.g. for the production of proteins (including  
XX erythropoietin, growth hormone or granulocyte-colony stimulating factor)  
XX and drug discovery. The advantage of these methods are that endogenous  
XX genes including those associated with human disease and development, may  
XX be activated and isolated without prior knowledge of the sequence  
XX structure, function or expression profile of the genes being known  
XX  
SQ Sequence 6838 BP; 1679 A; 1669 C; 1709 G; 1781 T; 0 U; 0 Other;  
  
Query Match 95.8%; Score 500.8; DB 3; Length 6838;  
Best Local Similarity 98.5%; Pred. No. 4.1e-165;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
  
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTAAGTACA 60  
Db 1300 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTAAGTACA 1359  
  
QY 61 ACAGGCAAGCTTGCACGCAATTCGATGAGAAATCTGCTTAGGTTAGGGGTTTTCGG 120  
Db 1360 ACAGGCAAGCTTGCACGCAATTCGATGAGAAATCTGCTTAGGTTAGGGGTTTTCGG 1419  
  
QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 180  
Db 1420 CTGCTTCGCGATGACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTAGG 1479  
  
QY 181 CGAAAGCGGGCTTCGCTGTGTACGGGTTAGGAGTCCCTCAGATATAGTATTCGC 240  
Db 1480 CGCCACGCGGGCTTCGCTGTGTACGGGTTAGGAGTCCCTCAGATATAGTATTCGC 1539  
  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 300  
Db 1540 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCAACATGG 1599  
  
QY 301 TAAACGATGCTTACCAATCCCTTAAAGGAGAGAAAGACCGTGCATGCCGATGG 360  
Db 1600 TAAACGATGCTTACCAATCCCTTAAAGGAGAGAAAGACCGTGCATGCCGATGG 1659  
  
QY 361 TGAAGTAAGTGGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGTCTGACATGA 420  
Db 1660 TGAAGTAAGTGGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGTCTGACATGA 1719  
  
QY 421 TTGACCAACCACTAATTCGCAATTCGAGAGAT-ATTGTATTAAAGTCCCTAGCTCGAT 479  
Db 1720 TTGACCAACCACTAATTCGCAATTCGAGAGATATTGTATTAAAGTCCCTAGCTCGAT 1779  
  
QY 480 ACAATAAACGCCATTGACCAATTCACCAATTCGATGTCACCTC 523  
Db 1780 ACAATAAACGCCATTGACCAATTCACCAATTCGATGTCACCTC 1823  
  
RESULT 27  
ABL57333  
ID ABL57333 standard; DNA; 8902 BP.



CC polyadenylation signal. The methods, vectors and cells comprising the  
CC vectors may be used for the non-targeted activation and over-expression  
CC of endogenous genes, e.g. for the production of proteins (including  
CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)  
CC and drug discovery. The advantage of these methods are that endogenous  
CC genes including those associated with human disease and development, may  
CC be activated and isolated without prior knowledge of the sequence  
CC structure, function or expression profile of the genes being known  
XX  
SQ Sequence 9725 BP; 2425 A; 2507 C; 2448 G; 2343 T; 0 U; 2 Other;  
Query Match 95.8%; Score 500.8; DB 3; Length 9725;  
Best Local Similarity 98.5%; Pred. No. 4.9e-165;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
XX  
QY 1 CTGCTCCCTGCTGTGTGTGGAGTCTGCTGAGTGTGCGGAGGCAAAATTAAGCTACA 60  
DB 1149 CTGCTCCCTGCTGTGTGTGGAGTCTGCTGAGTGTGCGGAGGCAAAATTAAGCTACA 1208  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGCTTAGCGTTTGGC 120  
DB 1209 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGCTTAGCGTTTGGC 1268  
QY 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTTTAGG 180  
DB 1269 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTTTAGG 1328  
QY 181 CGAAAGCGGGCTTCGCTTACGCGGTTAGGATCCCTCAGATATAGTACTTTCGC 240  
DB 1329 CGCCACGCGGGCTTCGCTTACGCGGTTAGGATCCCTCAGATATAGTACTTTCGC 1388  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
DB 1389 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1448  
QY 301 TAAAGCATGAGTATAGCAATGCTTTACAAGGAGAGAAAGCAACCGTGATGCCGATGG 360  
DB 1449 TAAAGCATGAGTATAGCAATGCTTTACAAGGAGAGAAAGCAACCGTGATGCCGATGG 1508  
QY 361 TGAAGTAAGTGTACGATCGCTCTATTAGGAGGACACAGCGGTCTGACATGGA 420  
DB 1509 TGAAGTAAGTGTACGATCGCTCTATTAGGAGGACACAGCGGTCTGACATGGA 1568  
QY 421 TTGACGACGACCTAATTCGCAATTCGACATGACAGAT-ATTGTATTAAAGTCCCTAGCTCGAT 479  
DB 1569 TTGACGACGACCTAATTCGCAATTCGCAATTCGACAGAT-ATTGTATTAAAGTCCCTAGCTCGAT 1628  
QY 480 ACAATAAACGCCATTGTGACCAATTCACCAATTTGGTGTGACCTC 523  
DB 1629 ACAATAAACGCCATTGTGACCAATTCACCAATTTGGTGTGACCTC 1672  
RESULT 29  
AAAS3879  
ID AAAS3879 standard; DNA; 9732 BP.  
XX  
AC AAAS3879;  
XX  
DT 03-JAN-2001 (first entry)  
XX  
DE Expression vector pRIG-TP.  
XX  
KW Vector; endogenous gene; activation; over-expression; erythropoietin;  
KW growth hormone; drug discovery; granulocyte colony stimulating factor;  
KW ds.  
XX  
OS Synthetic.  
XX  
PN WO200049162-A2.  
XX  
PD 24-AUG-2000.  
XX  
PF 22-FEB-2000; 2000WO-US004429.

XX 19-FEB-1999; 99US-00253022.  
PR 08-MAR-1999; 99US-00263814.  
PR 26-MAR-1999; 99US-00276820.  
XX  
XX (ATHE-) ATHERSYS INC.  
XX  
XX Harrington JU, Sherf B, Rundlett S;  
XX  
XX WPI; 2000-549276/50.  
XX  
XX Non-targeted activation of endogenous genes, e.g. for the production of  
PT erythropoietin, growth hormone or granulocyte-colony stimulating factor  
PT proteins and for drug discovery.  
XX  
XX Example 15; Fig 37; 240pp; English.  
XX  
XX New methods, vectors and cells are described for non-targeted activation  
CC and over-expression of endogenous genes. The vector constructs comprise  
CC transcriptional regulatory sequences (TRS) and unpaired splice donor  
CC sequences (USDS), preferably the vectors comprise (in sequential order) a  
CC TRS, an USDS, a rare cutting restriction site (RCS) and a linearization  
CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a  
CC polyadenylation signal. The methods, vectors and cells comprising the  
CC vectors may be used for the non-targeted activation and over-expression  
CC of endogenous genes, e.g. for the production of proteins (including  
CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)  
CC and drug discovery. The advantage of these methods are that endogenous  
CC genes including those associated with human disease and development, may  
CC be activated and isolated without prior knowledge of the sequence  
CC structure, function or expression profile of the genes being known  
XX  
SQ Sequence 9732 BP; 2427 A; 2512 C; 2443 G; 2348 T; 0 U; 2 Other;  
Query Match 95.8%; Score 500.8; DB 3; Length 9732;  
Best Local Similarity 98.5%; Pred. No. 4.9e-165;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
XX  
QY 1 CTGCTCCCTGCTGTGTGTGGAGTCTGCTGAGTGTGCGGAGGCAAAATTAAGCTACA 60  
DB 1152 CTGCTCCCTGCTGTGTGTGGAGTCTGCTGAGTGTGCGGAGGCAAAATTAAGCTACA 1211  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGCTTAGCGTTTGGC 120  
DB 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAGATCTGCTTAGGCTTAGCGTTTGGC 1271  
QY 121 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTTTAGG 180  
DB 1272 CTGCTTCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTCTTTAGG 1331  
QY 181 CGAAAGCGGGCTTCGCTTACGCGGTTAGGATCCCTCAGATATAGTACTTTCGC 240  
DB 1332 CGCCACGCGGGCTTCGCTTACGCGGTTAGGATCCCTCAGATATAGTACTTTCGC 1391  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
DB 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1451  
QY 301 TAAAGCATGAGTATAGCAATGCTTTACAAGGAGAGAAAGCAACCGTGATGCCGATGG 360  
DB 1452 TAAAGCATGAGTATAGCAATGCTTTACAAGGAGAGAAAGCAACCGTGATGCCGATGG 1511  
QY 361 TGAAGTAAGTGTACGATCGCTCTATTAGGAGGACACAGCGGTCTGACATGGA 420  
DB 1512 TGAAGTAAGTGTACGATCGCTCTATTAGGAGGACACAGCGGTCTGACATGGA 1571  
QY 421 TTGACGACGACCTAATTCGCAATTCGACATGACAGAT-ATTGTATTAAAGTCCCTAGCTCGAT 479  
DB 1572 TTGACGACGACCTAATTCGCAATTCGCAATTCGACAGAT-ATTGTATTAAAGTCCCTAGCTCGAT 1631  
QY 480 ACAATAAACGCCATTGTGACCAATTCACCAATTTGGTGTGACCTC 523  
DB 1632 ACAATAAACGCCATTGTGACCAATTCACCAATTTGGTGTGACCTC 1675

QY	181	CGAAAAACCGGGGCTTCGGTTGTACGCGGTTAGAGATCCCTCAGGATATAGTAGTTTCGC	240
Db	1471	CGCCCCAGCGGGGCTTCGGTTGTACGCGGTTAGAGATCCCTCAGGATATAGTAGTTTCGC	1530
QY	241	TTTTTGATAGGAGAGGGGAAATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGG	300
Db	1531	TTTTTGATAGGAGAGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTTGCAACATGG	1590
QY	301	TAAAGATAGTTAGCAACATGCCTTACAGGAGAGAAAGCACCGTGCAATGCCGATTGG	360
Db	1591	TAAAGATAGTTAGCAACATGCCTTACAGGAGAGAAAGCACCGTGCAATGCCGATTGG	1650
QY	361	TGGAAAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACAGGCTGCAATGGA	420
Db	1651	TGGAAAGTAAAGTGGTACGATCGTGCCTTATTAGGAGGCAACAGACAGGCTGCAATGGA	1710
QY	421	TTGCGAGCAACCACTAAATTCGCGATTTGCAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT	479
Db	1711	TTGCGAGCAACCACTAAATTCGCGATTTGCAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT	1770
QY	480	ACATATACACCCATTGTGACCATTCACACATTTGGTGTGCACCTC	523
Db	1771	ACATATACACCCATTGTGACCATTCACACATTTGGTGTGCACCTC	1814
RESULT 31			
ID	AAV59501 standard; DNA; 11265 BP.		
XX	AAV59501;		
AC	AC		
XX	17-OCT-2003 (revised)		
DT	02-FEB-1999 (first entry)		
DT	XX		
DE	Plasmid pREP7::CTLA4-hlg.		
XX	pREP7::CTLA4-hlg; plasmid; CTLA4; immunoglobulin; vaccine;		
KW	DNA immunisation; human; mouse; ds; circular; cyclic.		
OS	Homo sapiens.		
OS	Mus sp.		
OS	Chimeric.		
XX	W09844129-A1.		
PN	08-OCT-1998.		
PD	XX		
PF	26-MAR-1998; 98WO-AU000208.		
XX	XX		
PR	27-MAR-1997; 97AU-00005891.		
PR	13-FEB-1998; 98AU-00001830.		
XX	XX		
XX	{COIN-} COUNCIL QUEENSLAND INST MEDICAL RES.		
PA	{CSR-} COMMONWEALTH SCI & IND RES ORG.		
PA	{UYME-} UNIV MELBOURNE.		
PA	{HALL-} HALL INST MEDICAL RES WALTER & ELIZA.		
PA	{CSLC-} CSL LTD.		
XX	Boyle JS, Brady JL, Lew AM;		
PT	WPI; 1998-557122/47.		
DE	XX		
XX	DNA molecule for raising an immune response to antigen - comprises		
PT	sequence encoding dimerisation or multimerisation polypeptide.		
XX	XX		
PS	Disclosure; Page 32-37; 64pp; English.		
XX	XX		
CC	This is the DNA sequence of expression plasmid pREP7::CTLA4-hlg that		
CC	encodes a secreted form of the Fc fragment of human IgG1 fused to murine		
CC	CTLA4. The invention provides a new DNA molecule for use in raising an		
CC	immune response to an antigen. The DNA molecule comprises: (i) a first		
CC	sequence encoding a targeting molecule (e.g. CTLA4, which acts as a		
CC	targeting molecule to antigen-presenting cells expressing B-7); (ii) a		

[illegible]

D

1572 TTGGACGAACCACTGGAATTCGGCATTCGAGAGATATAATGATATATTCAGCGGCTTTT

QY 480 ACAATAAGCCGCTTACCAATTCACACATTTGGTGTGCACCTC 523  
DB 1632 ACAATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 33  
AAAS3876  
ID AAAS3876 standard; DNA; 10054 BP.  
AC AAAS3876;  
XX  
DT 03-JAN-2001 (first entry)  
DE Expression vector pRIGdb1.  
XX  
KW Vector; endogenous gene; activation; over-expression; erythropoietin;  
KW growth hormone; drug discovery; granulocyte colony stimulating factor;  
KW ds.  
XX  
OS Synthetic.  
XX  
PN WO200049162-A2.  
XX  
PD 24-AUG-2000.  
XX  
PF 22-FEB-2000; 2000WO-US004429.  
XX  
PR 19-FEB-1999; 99US-00253022.  
PR 08-MAR-1999; 99US-00263814.  
PR 26-MAR-1999; 99US-00276820.  
XX  
PA (ATHE-) ATHERSYS INC.  
XX  
PI Harrington J, Sherf B, Rundlett S;  
XX  
DR WPI; 2000-549276/50.  
XX  
PT Non-targeted activation of endogenous genes, e.g. for the production of  
PT erythropoietin, growth hormone or granulocyte-colony stimulating factor  
PT proteins and for drug discovery.  
XX  
PS Disclosure; Fig 33; 240pp; English.  
XX  
CC New methods, vectors and cells are described for non-targeted activation  
CC and over-expression of endogenous genes. The vector constructs comprise  
CC transcriptional regulatory sequences (TRS) and unpaired splice donor  
CC sequences (USDS), preferably the vectors comprise (in sequential order) a  
CC TRS, a rare cutting restriction site (RCRS) and a linearization  
CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a  
CC polyadenylation signal. The methods, vectors and cells comprising the  
CC vectors may be used for the non-targeted activation and over-expression  
CC of endogenous genes, e.g. for the production of proteins (including  
CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)  
CC and drug discovery. The advantage of these methods are that endogenous  
CC genes including those associated with human disease and development, may  
CC be activated and isolated without prior knowledge of the sequence  
CC structure, function or expression profile of the genes being known  
XX  
SQ Sequence 10054 BP; 2548 A; 2562 C; 2515 G; 2427 T; 0 U; 2 Other;

Query Match 93.5%; Score 488.8; DB 3; Length 10054;  
Best Local Similarity 98.3%; Pred. No. 8.6e-161;  
Matches 515; Conservative 0; Mismatches 7; Indels 2; Gaps 2;  
1 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTCGCGGACCAAAATTTAGCTACA 60  
DB 1475 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTCGCGGACCAAAATTTAGCTACA 1534  
QY 61 ACAAGGCAAGCTTGACCAATTCGATGCAATTCGATGAGGTGAGGCTTTTGGC 120  
DB 1535 ACAAGGCAAGCTTGACCAATTCGATGCAATTCGATGAGGTGAGGCTTTTGGC 1593  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 180

DB 1594 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 1653  
QY 181 CGAAAGCGGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTTGCG 240  
DB 1654 CGCCAGCGGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTTGCG 1713  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTTAGTGTGCAACATGG 300  
DB 1714 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTTAGTGTGCAACATGG 1773  
QY 301 TAACGATGATTTAGCAATGCTTACAGGAGAGAAAGACACCTGCAATCCGATTTGG 360  
DB 1774 TAACGATGATTTAGCAATGCTTACAGGAGAGAAAGACACCTGCAATCCGATTTGG 1833  
QY 361 TGGAGGTAGAGGTGTACGATGCTGCTTATTAGGAGGCAACAGCGGTCTGACATGGA 420  
DB 1834 TGGAGGTAGAGGTGTACGATGCTGCTTATTAGGAGGCAACAGCGGTCTGACATGGA 1893  
QY 421 TTGGACGACCACTAAATTCGCAATTCGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479  
DB 1894 TTGGACGACCACTAAATTCGCAATTCGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 1953  
QY 480 ACAATAAAGCCCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 523  
DB 1954 ACAATAAAGCCCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 1997

RESULT 34  
AAT71261  
ID AAT71261 standard; DNA; 565 BP.  
XX  
AC AAT71261;  
XX  
DT 30-MAR-1998 (first entry)  
XX  
DE Rous sarcoma virus v-src gene.  
XX  
KW Cognate transgene; v-src gene; lymphoma; cellular immunogen; cancer;  
KW self-determinant immunoreactivity; cancer vaccination; breast carcinoma;  
KW colon carcinoma; immunotherapy; proto-oncogene; rous sarcoma virus; ss.  
XX  
OS Rous sarcoma virus.  
XX  
PN WO9725860-A1.  
XX  
PD 24-JUL-1997.  
XX  
PF 13-JAN-1997; 97WO-US0000582.  
XX  
PR 19-JAN-1996; 96US-0010262P.  
XX  
PI (UYAL-) UNIV ALLEGHENY HEALTH SCI.  
XX  
PI Halpern MS, England JM;  
XX  
DR WPI; 1997-384993/35.  
XX  
PT Proto-oncogene immunogen - used in vaccine for the prevention and  
PT treatment of cancer.  
XX  
PS Disclosure; Page 69; 81pp; English.  
XX  
CC This sequence represents the Rous sarcoma virus v-src cognate transgene  
CC (CTG). Deletion of amino acids 430-433 of the encoded protein renders the  
CC CTG non-transforming. This sequence can be used in the cellular immunogen  
CC of the invention. The cellular immunogen of the invention is for  
CC immunising against the product of a target proto-oncogene, over-  
CC expression of which is associated with cancer, comprises host cells  
CC transfected with a construct containing at least one transgene related to  
CC the proto-oncogene and driven by a strong promoter. The product of the  
CC transgene induces immunoreactivity to host self-determinants on the  
CC product of proto-oncogene. The cellular immunogens are used for

XX

59077

RESULT 36  
AAA59077

ID AAA59077 standard; DNA; 11600 BP.  
XX  
AC AAA59077;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE Nucleotide sequence of plasmid pMNeoE2a-3.1.  
XX  
KW Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;  
KW ss.  
XX  
OS Synthetic.  
XX  
PN WO200042208-A1.  
XX  
PD 20-JUL-2000.  
XX  
PF 14-JAN-2000; 2000WO-EP000265.  
XX  
PR 14-JAN-1999; 99US-0115920P.  
XX  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-BRFINDUNGEN VERW GES MBH.  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Nemerow GR, Von Seggern DJ, Hallenbeck FL, Stevenson SC;  
PI Skripchenko Y;  
PI  
XX  
DR WPI; 2000-476069/41.  
XX  
XX New nucleic acid comprising an adenovirus tripartite leader nucleotide  
XX for producing high-capacity and targeted vectors for adenovirus-based  
XX gene therapy.  
XX  
XX Example 6; Page 192-195; 212pp; English.  
XX  
XX The specification describes a nucleic acid molecule comprising an  
XX adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence  
XX comprising two different TPL exons or three same or different TPL exons.  
XX The nucleic acid is used to produce an adenovirus vector particle,  
XX deliver an exogenous gene to a target cell, pseudotype recombinant viral  
XX vectors, target an adenovirus vector to a cell, produce a modified  
XX adenovirus, deliver a heterologous gene to an animal and produce a  
XX gutless adenoviral vector particle. The present sequence represents  
XX plasmid pMNeoE2a-3.1, which is used in the course of the invention  
XX  
SQ Sequence 11600 BP; 2929 A; 2747 C; 3012 G; 2912 T; 0 U; 0 Other;  
  
Query Match 82.4%; Score 430.8; DB 3; Length 11600;  
Best Local Similarity 99.5%; Pred. No. 2.6e-140;  
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 CTGCTCCCTGCTTGTGTGAGGTGCTGAGTAGTGTGCGGAGCAAAATTAAGCTACA 60  
Db 11167 CTGCTCCCTGCTTGTGTGAGGTGCTGAGTAGTGTGCGGAGCAAAATTAAGCTACA 11225  
  
QY 61 ACAAGGCAAGCTTGACCAAAATTCATCAAGATCTGCTAGGTTAGGCTTTGCG 120  
Db 11227 ACAAGGCAAGCTTGACCAAAATTCATCAAGATCTGCTAGGTTAGGCTTTGCG 11286  
  
QY 121 CTGCTTCGATGTAGCGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180  
Db 11287 CTGCTTCGATGTAGCGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 11346  
  
QY 181 CGAAAGCGGGCTTCGGTTGACCGGTTAGAGTCCCTTCAGATATAGTAGTTTCCG 240  
Db 11347 CGAAAGCGGGCTTCGGTTGACCGGTTAGAGTCCCTTCAGATATAGTAGTTTCCG 11406  
  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCATATCTTCTAGTCTTGCACATGG 300  
Db 11407 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCATATCTTCTAGTCTTGCACATGG 11466  
  
QY 301 TAACGATGAGTTAGCAACATGCTTTACAGAGAGAGAAAAGCAGCGTGCATGCCGATTGG 360

Db 11467 TAACGATGAGTTAGCAACATGCTTTACAGAGAGAGAAAAGCAGCGTGCATGCCGATTGG 11526  
  
QY 361 TCGAAGTAAAGTGTGATCGATCGTCCCTTTATAGGAGGCAACAGCGGCTTGCATGGA 420  
Db 11527 TCGAAGTAAAGTGTGATCGATCGTCCCTTTATAGGAGGCAACAGCGGCTTGCATGGA 11586  
  
QY 421 TTGGACGACCACT 434  
Db 11587 TTGGACGACCACT 11600  
  
RESULT 37  
ABA94279  
ID ABA94279 standard; DNA; 11600 BP.  
XX  
AC ABA94279;  
XX  
DT 13-MAR-2002 (first entry)  
XX  
DE Nucleotide sequence of plasmid WMTV-E2a-SV40-Neo.  
XX  
KW Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease;  
KW fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STDGI;  
KW ophthalmological; antiinflammatory; antidiabetic; cytostatic;  
KW gene therapy; tripartite leader; TPL; ss.  
XX  
OS Synthetic.  
XX  
PN WO200183729-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 30-APR-2001; 2001WO-EP004863.  
XX  
PR 01-MAY-2000; 2000US-00562934.  
XX  
XX (NOVS ) NOVARTIS AG.  
XX (SCRI ) SCRIPPS RES INST.  
XX (NEME/) NEMEROW G R.  
XX (VSEG/) VON SEGGERN D J.  
XX (FRIE/) FRIEDLANDER M.  
XX  
PI Nemerow GR, Von Seggern DJ, Friedlander M;  
PI  
XX  
DR WPI; 2002-082846/11.  
XX  
XX Polynucleotide for making vectors, useful for treating ocular diseases,  
XX e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat  
XX sequences, packaging signal and photoreceptor-specific promoter.  
XX  
XX Example 5; Page 141-145; 149pp; English.  
XX  
XX The invention provides an isolated polynucleotide comprising adenovirus  
XX (AV) inverter terminal repeat sequences (ITRS), AV packaging signal  
XX operatively linked to ITRS and a photoreceptor-specific promoter. A  
XX recombinant AV vector (AVV) comprising the polynucleotide is useful for  
XX targeted delivery of a gene product to the eye (especially to the  
XX vitreous cavity), for treating an ocular disease, e.g., retinal  
XX degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic  
XX retinopathies, retinal vascularizations, and retinoblastoma, of a mammal  
XX preferably human. The AAV comprises a fiber protein that specifically or  
XX selectively binds to receptors that are expressed on cells (preferably  
XX photoreceptors in the eye). Preferably, the recombinant virus comprise a  
XX fiber protein from an adenovirus type B subgroup or is a chimeric protein  
XX containing a portion of the N-terminus of an adenovirus type 2 or type 5  
XX penton, and the therapeutic product is a trophic factor, an anti-  
XX apoptotic factor, gene encoding a rhodopsin protein, a wild-type  
XX stargardt disease gene (STDGI), an anti-cancer agent and a protein that  
XX regulates expression of a photoreceptor specific gene product. The viral  
XX nucleic acid of AAV comprises ITRS and packaging signal derived from AAV  
XX subgroup B or C, especially an AV type 2 or type 5. AAV is also useful  
XX for targeted gene therapy, where the vector comprises an AV type 37 fiber



CC protein or its portion, and selectively transduces photoreceptors and  
 CC delivers a gene product encoded by AAV. The present sequence represents  
 CC the nucleotide sequence of plasmid MMTV-E2a-SV40-Neo  
 XX  
 SQ Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;  
 Query Match 82.4%; Score 430.8; DB 6; Length 11600;  
 Best Local Similarity 99.5%; Pred. No. 2.6e-140; Indels 0; Gaps 0;  
 Matches 432; Conservative 0; Mismatches 2;  
 1 CTGCTCCCTGCTTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
 11167 CTGCTCCCTGCTTGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 11226  
 61 ACAAGCCAGGCTTGACCGCAATTCGATGAGAACTCTGCTTAGGCTTAGGCTTTGCG 120  
 11227 ACAAGCCAGGCTTGACCGCAATTCGATGAGAACTCTGCTTAGGCTTAGGCTTTGCG 11286  
 121 CTGCTTCGCGATGTACGGCCAGATATTCGGGTATCTGAGGCACTAGGGTGTGTTAGG 180  
 11287 CTGCTTCGCGATGTACGGCCAGATATTCGGGTATCTGAGGCACTAGGGTGTGTTAGG 11346  
 181 CGAAAAGCGGGCTTCGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTTTCCG 240  
 11347 CGAAAAGCGGGCTTCGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTTTCCG 11406  
 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 11407 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 11466  
 301 TAACGATGAGTGTAGCAATGCTTACAGGAGAGAAAGCAACCGTGCATGCGATTGG 360  
 11467 TAACGATGAGTGTAGCAATGCTTACAGGAGAGAAAGCAACCGTGCATGCGATTGG 11526  
 361 TGGAGTAAAGTGTGACGATCGTCTTATTAGGAGGCAACAGCGGTCTGACATGGA 420  
 11527 TGGAGTAAAGTGTGACGATCGTCTTATTAGGAGGCAACAGCGGTCTGACATGGA 11586  
 421 TTGGACGAACCACT 434  
 11587 TTGGACGAACCACT 11600  
 RESULT 38  
 AAL56865  
 ID AAL56865 standard; DNA; 11600 BP.  
 XX  
 AC AAL56865;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE DNA sequence of the plasmid MMTV-E2a-SV40-Neo construct.  
 XX  
 KW Fibre shaft modification; adenoviral vector; cell entry pathway; penton;  
 KW CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;  
 KW gene therapy; fibre knob; ds.  
 XX  
 OS Rhesus macaque polyoma virus.  
 OS Unidentified adenovirus.  
 OS Unidentified.  
 XX  
 FN WO2003062400-A2.  
 XX  
 PD 31-JUL-2003.  
 XX  
 PF 24-JAN-2003; 2003WO-US002295.  
 XX  
 PR 24-JAN-2002; 2002US-0350388P.  
 PR 26-JUN-2002; 2002US-0331967P.  
 XX  
 PA (SCRI) SCRIPPS RES INST.  
 PA (NOVS) NOVARTIS AG.  
 XX

PI Kaleko M, Nemerow GR, Smith T, Stevenson SC;  
 XX WPI; 2003-627459/59.  
 XX New modified adenovirus capsid protein, useful as a base vector for  
 PT producing redirected adenoviruses.  
 XX  
 PS Disclosure; Page 143-146; 132pp; English.  
 XX  
 CC This invention relates to novel fibre shaft modifications in adenoviral  
 CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a  
 CC specific targeted tissue or organ, accordingly gene therapy requires the  
 CC ablation of normal virus tropism. If successful, systemic vector delivery  
 CC into a peripheral vein would be targeted to the desired location in the  
 CC body without any associated side effects, which would permit lower, less  
 CC toxic vector doses that are also potentially less immunogenic. The  
 CC present invention describes capsid modifications, specifically fibre  
 CC shaft mutations that when expressed on adenoviral particles ablated  
 CC binding to heparin sulphate proteoglycans (HSP) thus providing targeted  
 CC vectors. Furthermore, when this is combined with modifications of other  
 CC adenoviral proteins involved in the cell entry pathway such as the fibre  
 CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors  
 CC become fully detargeted. As such, these fully ablated particles can be  
 CC used in vivo as base vectors for producing redirected adenoviruses with  
 CC the desired cell specificity. This polynucleotide sequence is the plasmid  
 CC MMTV-E2a-SV40-Neo construct used to provide complementation of the  
 CC adenoviral E2a function of the invention  
 XX  
 SQ Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;  
 Query Match 82.4%; Score 430.8; DB 8; Length 11600;  
 Best Local Similarity 99.5%; Pred. No. 2.6e-140; Indels 0; Gaps 0;  
 Matches 432; Conservative 0; Mismatches 2;  
 1 CTGCTCCCTGCTTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
 11167 CTGCTCCCTGCTTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 11226  
 61 ACAAGCCAGGCTTGACCGCAATTCGATGAGAACTCTGCTTAGGCTTAGGCTTTGCG 120  
 11227 ACAAGCCAGGCTTGACCGCAATTCGATGAGAACTCTGCTTAGGCTTAGGCTTTGCG 11286  
 121 CTGCTTCGCGATGTACGGCCAGATATTCGGGTATCTGAGGCACTAGGGTGTGTTAGG 180  
 11287 CTGCTTCGCGATGTACGGCCAGATATTCGGGTATCTGAGGCACTAGGGTGTGTTAGG 11346  
 181 CGAAAAGCGGGCTTCGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTTTCCG 240  
 11347 CGAAAAGCGGGCTTCGGTGTGACGGGTAGGAGTCCCTCAGGATATAGTTTCCG 11406  
 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 11407 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 11466  
 301 TAACGATGAGTGTAGCAATGCTTACAGGAGAGAAAGCAACCGTGCATGCGATTGG 360  
 11467 TAACGATGAGTGTAGCAATGCTTACAGGAGAGAAAGCAACCGTGCATGCGATTGG 11526  
 361 TGGAGTAAAGTGTGACGATCGTCTTATTAGGAGGCAACAGCGGTCTGACATGGA 420  
 11527 TGGAGTAAAGTGTGACGATCGTCTTATTAGGAGGCAACAGCGGTCTGACATGGA 11586  
 421 TTGGACGAACCACT 434  
 11587 TTGGACGAACCACT 11600  
 RESULT 39  
 ADB75125  
 ID ADB75125 standard; DNA; 11600 BP.  
 XX  
 AC ADB75125;  
 XX

DT 04-DEC-2003 (first entry)  
 XX Chromosomal insertion pMNeOE2a-3.1.  
 DE  
 XX ophthalmological; antiinflammatory; antidiabetic; gene therapy;  
 KW adenovirus inverted terminal repeat sequence;  
 KW adenovirus packaging signal; photoreceptor-specific promoter;  
 KW adenovirus type 37; adenovirus type D serotype; adenovirus type 2;  
 KW adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor;  
 KW rhodopsin; wild-type Stargardt disease gene; STG1; anti-cancer agent;  
 KW retinal degenerative disease; retinitis pigmentosa; Stargardt's disease;  
 KW diabetic retinopathy; retinal vascularisation; choroideraemia;  
 KW gyrate atrophy; macular dystrophy; retinoblastoma;  
 KW photoreceptor-restricted transgene expression;  
 KW recombinant adenovirus vector; adenovirus type 5; E2a;  
 KW chromosomal insertion; ds.  
 XX Homo sapiens.  
 OS  
 XX US2002193327-A1.  
 PN  
 XX 19-DEC-2002.  
 PD  
 XX  
 XX 01-MAY-2001; 2001US-00847101.  
 PF  
 XX  
 XX 01-MAY-2000; 2000US-00562934.  
 PR  
 XX (Scri ) SCRIPPS RES INST.  
 PA  
 XX  
 XX Nemerow GR, Von Seggern DJ, Friedlander M;  
 FI  
 XX WPI; 2003-657234/62.  
 DR  
 XX Novel nucleic acids comprising adenovirus inverted terminal repeat  
 PT sequences, adenovirus packaging signals operatively linked to the  
 PT sequences and photoreceptor-specific promoters, useful for treating  
 PT retinitis pigmentosa.  
 PT  
 XX Example 5; Page 93-98; 106pp; English.  
 PS  
 XX The invention describes an isolated nucleic acid (I) comprising  
 CC adenovirus inverted terminal repeat sequence, and an adenovirus packaging  
 CC signal operatively linked to the sequence, and a photoreceptor-specific  
 CC promoter. A recombinant adenovirus vector (II) comprising (I) is useful  
 CC for targeted delivery of a gene product to the eye of a mammal which  
 CC involves administering (II) that comprises heterologous DNA encoding the  
 CC gene product or resulting in expression of the gene product, where the  
 CC recombinant virus comprises a fibre protein that specifically or  
 CC selectively binds to receptors that are expressed on cells which are  
 CC photoreceptors, in the eye. The recombinant virus comprises a fibre  
 CC protein which is an adenovirus type 37, from an adenovirus type D  
 CC serotype. The fibre is a chimeric protein containing a sufficient portion  
 CC of the N-terminus of an adenovirus type 2 or type 5 fibre protein for  
 CC interaction with an adenovirus type 2 or type 5 penton, and a sufficient  
 CC portion of an adenovirus serotype D knob portion of the fibre for  
 CC selective binding to photoreceptors in the eye of a mammal. The  
 CC encapsulated nucleic acid comprises a photoreceptor-specific promoter  
 CC operatively linked to a nucleic acid comprising the therapeutic product  
 CC which is chosen from trophic factor, anti-apoptotic factor, gene encoding  
 CC a rhodopsin protein, wild-type Stargardt disease gene (STG1), an anti-  
 CC cancer agent and a protein that regulates expression of a photoreceptor-  
 CC specific gene product. The delivery is effected for treatment of an  
 CC ocular disease such as retinal degenerative disease e.g., retinitis  
 CC pigmentosa, Stargardt's disease, diabetic retinopathies, retinal  
 CC vascularisation, choroideraemia, gyrate atrophy or macular dystrophy or  
 CC retinoblastoma inherited and acquired retinal and neovascular  
 CC degenerative diseases. The viral nucleic acid comprises an adenovirus  
 CC inverted terminal repeat (ITR) sequences, and an adenovirus packaging  
 CC signal operatively linked to the sequence. The ITRs and packaging signal  
 CC are derived from an adenovirus serotype B or C, or adenovirus type 2 or  
 CC 5. The viral nucleic acid further comprises a photoreceptor-specific  
 CC promoter. (II) includes photoreceptor promoters providing a means not  
 CC only for specific targeting of expression in these cells, but also for

CC photoreceptor-restricted transgene expression. This sequence represents a  
 CC chromosomal insertion found in adenoviral plasmids of the A519 lung  
 CC carcinoma cell line which provide a complement of adenoviral E2a gene  
 CC function.  
 XX  
 XX Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;  
 Query Match 82.4%; Score 430.8; DB 9; Length 11600;  
 Best Local Similarity 99.5%; Pred. No. 2.6e-140;  
 Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 CTGCTCCCTGCTTGTGTTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTTACA 60  
 Db 11167 CTGCTCCCTGCTTGTGTTGGAGGTGCTGAGTAGTGCAGGAGCAAAATTAAGCTTACA 11226  
 Qy 61 ACAAGGCAAGGCTTGCACGCAATTCATGAGAAATCTGTAGGGTTAGCGTTTGGCG 120  
 Db 11227 ACAAGGCAAGGCTTGCACGCAATTCATGAGAAATCTGTAGGGTTAGCGTTTGGCG 11286  
 Qy 121 CTGCTTCGGATGATACGGGCGCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 11347 CGAAAGCGGGGCTTCGTTGTAGCGGGTTAGGATGCCCTCAGGATATAGTAGTTTCGC 11406  
 Qy 241 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Db 11407 TTTTGCATAGGAGGGGGAAATGTAGTCTTATGCAATCACTTGTAGTCTTGCACATGG 11466  
 Qy 301 TACGATGATGATGACACATGCTTACAGGAGAGAAAAGACCGTCATGCCGATGG 360  
 Db 11467 TACGATGATGATGACACATGCTTACAGGAGAGAAAAGACCGTCATGCCGATGG 11526  
 Qy 361 TCGAAGTAAGTGTGATGATGCTGCTCTTATTAGGAGGCAACAGACGGTCTGCATGGA 420  
 Db 11527 TCGAAGTAAGTGTGATGATGCTGCTCTTATTAGGAGGCAACAGACGGTCTGCATGGA 11586  
 Qy 421 TTGGACGACCACT 434  
 Db 11587 TTGGACGACCACT 11600  
 RESULT 40  
 AAA14722  
 ID AAA14722 standard; DNA; 2187 BP.  
 AC AAA14722;  
 XX  
 XX 06-AUG-2003 (revised)  
 DT 08-AUG-2000 (first entry)  
 DE Nucleotide sequence of region A of vector Ad5RSVbeta-lactamase.  
 KW Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;  
 KW replication-deficient adenovirus type 5; suicide gene therapy;  
 KW cancer cell; chemotherapy; beta-lactamase producing enzyme; prodrug TCM;  
 KW anticancer; tumor; leukemia; breast cancer; Wilms tumor;  
 KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;  
 KW papillary adenocarcinoma; es.  
 XX  
 XX Synthetic.  
 OS Rous sarcoma virus.  
 OS Mastadenovirus.  
 XX WO2000020608-A1.  
 PN  
 XX 13-APR-2000.  
 PD  
 XX 01-OCT-1999; 99WO-US020908.  
 PF  
 XX 02-OCT-1998; 98US-00165321.  
 PR

XX (GENO-) GENOTHERAPEUTICS INC.  
 XX Steiner MS;  
 XX WPI; 2000-303788/26.  
 XX  
 XX Treating cancer using viral vectors which encode enzymes that convert  
 XX inactive drugs to active cytotoxic agents, expression of the enzyme is  
 XX tissue specific therefore targeting the effects of the drug to tumor  
 XX cells.  
 XX  
 XX Disclosure; Fig 10; 130pp; English.  
 XX  
 XX The specification describes a method for inducing cellular cytotoxicity  
 XX in tumor cells using replication-deficient adenovirus type 5 expression  
 XX vectors. The vectors comprise a sequence encoding a beta-lactamase under  
 XX the control of a Rous Sarcoma virus in combination with a prodrug  
 XX conjugated to a toxic agent. Tissue specific expression of the enzyme  
 XX converts the inactive drugs into active cancer killing agents. The  
 XX adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-  
 XX lactamase sequence is inserted within this region. The vectors are used  
 XX for suicide gene therapy. This involves introducing genes into cancer  
 XX cells that encode enzymes capable of converting inactive drugs into  
 XX active cancer killing agents. If tissue specific promoters are coupled to  
 XX the prodrug enzymes, then production of the prodrug will be tissue  
 XX specific and targeted to the tumor. Therefore the cancer cells act as  
 XX their own factories to activate chemotherapy agents and commit suicide.  
 XX Beta-lactamase prodrug enzymes convert prodrug TCM into an active  
 XX anticancer agent which is cytotoxic to cancer cells PPC-1. The method is  
 XX used to treat patients with cancers of the brain, bladder or prostate. It  
 XX may also be used to treat a range of other tumors such as leukemia,  
 XX breast cancer, Wilms' tumor, small cell lung carcinoma, Ewing's sarcoma,  
 XX colon carcinoma and papillary adenocarcinomas. The present sequence  
 XX represents region A of vector Ad5RSVbeta-lactamase, a vector of the  
 XX invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 XX Sequence 2187 BP; 562 A; 477 C; 592 G; 556 T; 0 U; 0 Other;  
 XX  
 XX Query Match 75.1%; Score 393; DB 3; Length 2187;  
 XX Best Local Similarity 98.8%; Pred. No. 2.4e-127;  
 XX Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 XX  
 QY 123 GCTTCGCGATGATACGGCGGCGAGATATTCGGGTATCTGAGGGGACTAGGGGTGTTAGGCG 182  
 Db 404 GCGCCCGATGATACGGCGGCGAGATATTCGGGTATCTGAGGGGACTAGGGGTGTTAGGCG 463  
 QY 183 AAAAGCGGGCTTCGGTGTACGGCGGTAGGAGTCCCTCAGGATATAGTATGCTTTCGCTT 242  
 Db 464 AAAAGCGGGCTTCGGTGTACGGCGGTAGGAGTCCCTCAGGATATAGTATGCTTTCGCTT 523  
 QY 243 TTGCATAGGAGGGGGGAATGATGCTTATGCAATATCTTGTAGTCTTTCGCAATGCTA 302  
 Db 524 TTGCATAGGAGGGGGGAATGATGCTTATGCAATATCTTGTAGTCTTTCGCAATGCTA 583  
 QY 303 ACGATGATGTAGCAATGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362  
 Db 584 ACGATGATGTAGCAATGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643  
 QY 363 GAAGTATAGGTGTAGCAATGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 422  
 Db 644 GAAGTATAGGTGTAGCAATGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703  
 QY 423 GGACGAGACCACTAAATTCGCGATTCGAGATATTTGATTTAAAGTCCCTAGCTCGATACA 482  
 Db 704 GGACGAGACCACTAAATTCGCGATTCGAGATATTTGATTTAAAGTCCCTAGCTCGATACA 763  
 QY 483 ATAAAGCCATTTGACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCAATTC 523  
 Db 764 ATAAAGCCATTTGACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCAATTC 804

AAZ93333  
 ID AAZ93333 standard; DNA; 2829 BP.  
 XX  
 XX AAZ93333;  
 XX  
 XX 04-JUL-2000 (first entry)  
 XX  
 XX Partial sequence of replication deficient adenoviral vector Ad5RSV2C9.  
 XX  
 XX Adenovirus; Vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 XX Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;  
 XX prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200014256-A1.  
 XX  
 XX 16-MAR-2000.  
 XX  
 XX 03-SEP-1999; 99WO-US018834.  
 XX  
 XX 04-SEP-1998; 98US-00148275.  
 XX  
 XX (GENO-) GENOTHERAPEUTICS INC.  
 XX  
 XX Steiner MS, Lu Y;  
 XX  
 XX WPI; 2000-257001/22.  
 XX  
 XX Replication-deficient adenovirus type 5 expression vectors used for gene  
 XX therapy of cancer, especially prostate cancer, comprising an insertion of  
 XX nucleic acid encoding cytochrome p450 genes.  
 XX  
 XX Claim 16; Fig 11A; 110pp; English.  
 XX  
 XX Replication-deficient adenovirus type 5 expression vectors comprise an  
 XX adenovirus genome with a deletion in the E1 and E2 region of the genome  
 XX and an insertion within the region under the control of a Rous Sarcoma  
 XX virus promoter can be used to induce chemotoxicity in tumour cells. Three  
 XX such expression vectors are described, the inserted nucleic acids in each  
 XX being the following: Vector (I) has an insertion of a nucleic acid  
 XX encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-  
 XX 2628). Vector (II) has an insertion of a nucleic acid encoding a  
 XX cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector  
 XX (III) has an insertion of a nucleic acid encoding a nicotinamide adenine  
 XX dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is  
 XX designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell  
 XX can be induced by administering (I) and (III) or (II) and (III) into the  
 XX tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell  
 XX to a prodrug and then administering the prodrug which kills the cell,  
 XX inducing its chemotoxicity. The method uses gene-directed enzyme prodrug  
 XX therapy to transfer a drug susceptibility gene to the tumor which can kill  
 XX activates a nontoxic prodrug intratumorally so the released drug can kill  
 XX the tumor cells containing the drug susceptibility gene. This sequence is  
 XX designated region A of the vector Ad5RSV2C9 and is the sequence of the  
 XX cytochrome 2C9 p450  
 XX  
 XX Sequence 2829 BP; 748 A; 633 C; 707 G; 741 T; 0 U; 0 Other;  
 XX  
 XX Query Match 75.1%; Score 393; DB 3; Length 2829;  
 XX Best Local Similarity 98.8%; Pred. No. 2.7e-127;  
 XX Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 XX  
 QY 123 GCTTCGCGATGATACGGCGGCGAGATATTCGGGTATCTGAGGGGACTAGGGGTGTTAGGCG 182  
 Db 404 GCGCCCGATGATACGGCGGCGAGATATTCGGGTATCTGAGGGGACTAGGGGTGTTAGGCG 463  
 QY 183 AAAAGCGGGCTTCGGTGTACGGCGGTAGGAGTCCCTCAGGATATAGTATGCTTTCGCTT 242  
 Db 464 AAAAGCGGGCTTCGGTGTACGGCGGTAGGAGTCCCTCAGGATATAGTATGCTTTCGCTT 523  
 QY 243 TTGCATAGGAGGGGGGAATGATGCTTATGCAATATCTTGTAGTCTTTCGCAATGCTA 302

Db 524 TTGCTATGGGAGGGGAATGTAGCTTATGCAATCTTGTAGTCTGCAACATGGTA 583  
 Qy 303 ACGATGATTAGCAATGCTTACAGGAGAGAAAGACCACTGCTGATGCCGATGGTG 362  
 Db 584 ACGATGATTAGCAATGCTTACAGGAGAGAAAGACCACTGCTGATGCCGATGGTG 643  
 Qy 363 GAGTAAGGTGATGATGCTGCTTATAGGAAGGCAACAGCGGTCTGCAATGGATT 422  
 Db 644 GAGTAAGGTGATGATGCTGCTTATAGGAAGGCAACAGCGGTCTGCAATGGATT 703  
 Qy 423 GGACGAACCACTAAATTCGGCATTCAGAGATATTGTATTAAGTGGCTAGCTCGATACA 482  
 Db 704 GGACGAACCACTAAATTCGGCATTCAGAGATATTGTATTAAGTGGCTAGCTCGATACA 763  
 Qy 483 ATAAACGCCATTGACCAATTCACCAATTCGATGGTGTGCACCTC 523  
 Db 764 ATAAACGCCATTGACCAATTCACCAATTCGATGGTGTGCACCTC 804

RESULT 42  
 AAZ93078  
 ID AAZ93078 standard; DNA; 2878 BP.  
 XX  
 AC AAZ93078;  
 XX  
 DT 04-JUL-2000 (first entry)  
 XX  
 DE Partial sequence of replication deficient adenoviral vector Ad5RSV3A4.  
 XX  
 KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;  
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200014256-A1.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 03-SEP-1999; 99WO-US018834.  
 XX  
 PR 04-SEP-1998; 98US-00148275.  
 XX  
 PA (GENO-) GENOTHERAPEUTICS INC.  
 XX  
 PI Steiner MS, Lu Y;  
 XX  
 DR WPI; 2000-257001/22.  
 XX

XX  
 XX Claim 17; Fig 11B; 110pp; English.  
 XX  
 CC Replication-deficient adenovirus type 5 expression vectors comprise an  
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome  
 CC and an insertion within the region under the control of a Rous Sarcoma  
 CC virus promoter can be used to induce chemotoxicity in tumour cells. Three  
 CC such expression vectors are described, the inserted nucleic acids in each  
 CC being the following: Vector (I) has an insertion of a nucleic acid  
 CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-  
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a  
 CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector  
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine  
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is  
 CC designated Ad5RSVRPD (ATCC VR-2630). The chemotoxicity of a tumor cell  
 CC can be induced by administering (I) and (III) or (II) and (III) into the  
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell  
 CC to a prodrug and then administering the prodrug which kills the cell,  
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug  
 CC therapy to transfer a drug susceptibility gene to the tumor which  
 CC activates a nontoxic prodrug intratumorally so the released drug can kill

CC the tumor cells containing the drug susceptibility gene. This sequence is  
 CC designated region A of the vector Ad5RSV3A4 and is the sequence of the  
 CC cytochrome 3A4 p450  
 XX  
 SQ Sequence 2878 BP; 786 A; 609 C; 710 G; 773 T; 0 U; 0 Other;  
 Query Match 75.1%; Score 393; DB 3; Length 2878;  
 Best Local Similarity 98.8%; Pred. No. 2.7e-127;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Qy 123 GCTTCGCGATGTACGGGCGAGATATTCGCTATCTAGGGGACTAGGCTGTGTTAGGCG 182  
 Db 404 GCGCCCGGATGTACGGGCGAGATATACCGCTATCTAGGGGACTAGGCTGTGTTAGGCG 463  
 Qy 183 AAAAGCGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGCTT 242  
 Db 464 AAAAGCGGGGCTTCGGTTGTAGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGCTT 523  
 Qy 243 TTGCATAGGAGGGGGAATGTAGTCTTATCAATACCTTTGTAGTCTTTGCAACATGGTA 302  
 Db 524 TTGCATAGGAGGGGGAATGTAGTCTTATCAATACCTTTGTAGTCTTTGCAACATGGTA 583  
 Qy 303 ACGATGATTAGCAACATGCTTACAGGAGAGAAAGACCACTGCTGATGCCGATGGTG 362  
 Db 584 ACGATGATTAGCAACATGCTTACAGGAGAGAAAGACCACTGCTGATGCCGATGGTG 643  
 Qy 363 GAGTAAGGTGATGATGCTGCTTATAGGAAGGCAACAGCGGTCTGCAATGGATT 422  
 Db 644 GAGTAAGGTGATGATGCTGCTTATAGGAAGGCAACAGCGGTCTGCAATGGATT 703  
 Qy 423 GGACGAACCACTAAATTCGGCATTCAGAGATATTGTATTAAGTGGCTAGCTCGATACA 482  
 Db 704 GGACGAACCACTAAATTCGGCATTCAGAGATATTGTATTAAGTGGCTAGCTCGATACA 763  
 Qy 483 ATAAACGCCATTGACCAATTCACCAATTCGATGGTGTGCACCTC 523  
 Db 764 ATAAACGCCATTGACCAATTCACCAATTCGATGGTGTGCACCTC 804

RESULT 43  
 AAZ93331  
 ID AAZ93331 standard; DNA; 3310 BP.  
 XX  
 AC AAZ93331;  
 XX  
 DT 04-JUL-2000 (first entry)  
 XX  
 DE Partial sequence of replication deficient adenoviral vector Ad5RSVRed.  
 XX  
 KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;  
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200014256-A1.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 03-SEP-1999; 99WO-US018834.  
 XX  
 PR 04-SEP-1998; 98US-00148275.  
 XX  
 PA (GENO-) GENOTHERAPEUTICS INC.  
 XX  
 PI Steiner MS, Lu Y;  
 XX  
 DR WPI; 2000-257001/22.  
 XX  
 PT Replication-deficient adenovirus type 5 expression vectors used for gene  
 PT therapy of cancer, especially prostate cancer, comprising an insertion of  
 PT nucleic acid encoding cytochrome p450 genes.  
 XX

PS Disclosure; Fig 10; 110pp; English.

XX Replication-deficient adenovirus type 5 expression vectors comprise an  
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome  
 CC and an insertion within the region under the control of a Rous Sarcoma  
 CC virus promoter can be used to induce chemotoxicity in tumour cells. Three  
 CC such expression vectors are described, the inserted nucleic acids in each  
 CC being the following: Vector (I) has an insertion of a nucleic acid  
 CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-  
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a  
 CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector  
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine  
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is  
 CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell  
 CC can be induced by administering (I) and (III) or (II) and (III) into the  
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell  
 CC to a prodrug and then administering the prodrug which kills the cell,  
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug  
 CC therapy to transfer a drug susceptibility gene to the tumor which  
 CC activates a non-toxic prodrug intratumorally so the released drug can kill  
 CC the tumor cells containing the drug susceptibility gene. This sequence is  
 CC designated region A of the vector Ad5RSVRed

XX Sequence 3310 BP; 755 A; 881 C; 980 G; 694 T; 0 U; 0 Other;  
 SQ

Query Match 75.1%; Score 393; DB 3; Length 3310;  
 Best Local Similarity 98.8%; Pred. No. 2.9e-127;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGGATGTACGGCCAGATATTCGGTATCTGAGGAGTACGGTGTGTTAGCGG 182  
 Db GCGCCCCGATGTACGGCCAGATATTCGGTATCTGAGGAGTACGGTGTGTTAGCGG 463

QY 183 AAAAGCGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 242  
 Db AAAAGCGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 523

QY 243 TTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTATGCAATCTCTTATGCAATCTCTT 302  
 Db TTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTATGCAATCTCTTATGCAATCTCTT 583

QY 303 AGATAGGAGGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 362  
 Db AGATAGGAGGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 643

QY 363 GAAATAGGAGGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 422  
 Db GAAATAGGAGGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 703

QY 423 GACGAAACCACTAAATTCGGATTCGACATATTCGATATTCGATATTCGATATTCGATATTC 482  
 Db GACGAAACCACTAAATTCGGATTCGACATATTCGATATTCGATATTCGATATTCGATATTC 763

QY 483 ATAAACGCCATTTGACCACTTACCACTTACCACTTACCACTTACCACTTACCACTTACCACTT 523  
 Db ATAAACGCCATTTGACCACTTACCACTTACCACTTACCACTTACCACTTACCACTTACCACTT 804

RESULT 44  
 ID AA293079 standard; DNR; 3311 BP.  
 AC  
 XX  
 AC AA293079;  
 XX  
 DT 04-JUL-2000 (first entry)  
 XX  
 XX Partial sequence of replication deficient adenoviral vector Ad5RSVRed.  
 DE  
 XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;  
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX  
 OS Synthetic.

XX Replication-deficient adenovirus type 5 expression vectors comprise an  
 PN adenovirus genome with a deletion in the E1 and E2 region of the genome  
 PD and an insertion within the region under the control of a Rous Sarcoma  
 PD virus promoter can be used to induce chemotoxicity in tumour cells. Three  
 PF such expression vectors are described, the inserted nucleic acids in each  
 PF being the following: Vector (I) has an insertion of a nucleic acid  
 PR encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-  
 PR 2628). Vector (II) has an insertion of a nucleic acid encoding a  
 PR cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector  
 PR (III) has an insertion of a nucleic acid encoding a nicotinamide adenine  
 PA dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is  
 PA designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell  
 PA can be induced by administering (I) and (III) or (II) and (III) into the  
 PA tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell  
 PA to a prodrug and then administering the prodrug which kills the cell,  
 PI inducing its chemotoxicity. The method uses gene-directed enzyme prodrug  
 PI therapy to transfer a drug susceptibility gene to the tumor which  
 PI activates a non-toxic prodrug intratumorally so the released drug can kill  
 PT the tumor cells containing the drug susceptibility gene. This sequence is  
 PT designated region A of the vector Ad5RSVRed and is the sequence of the  
 PT cytochrome NADPH p450 reductase

XX Sequence 3311 BP; 755 A; 881 C; 981 G; 694 T; 0 U; 0 Other;  
 SQ

Query Match 75.1%; Score 393; DB 3; Length 3311;  
 Best Local Similarity 98.8%; Pred. No. 2.9e-127;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGGATGTACGGCCAGATATTCGGTATCTGAGGAGTACGGTGTGTTAGCGG 182  
 Db GCGCCCCGATGTACGGCCAGATATTCGGTATCTGAGGAGTACGGTGTGTTAGCGG 463

QY 183 AAAAGCGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 242  
 Db AAAAGCGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 523

QY 243 TTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTATGCAATCTCTTATGCAATCTCTT 302  
 Db TTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTATGCAATCTCTTATGCAATCTCTT 583

QY 303 AGATAGGAGGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 362  
 Db AGATAGGAGGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 643

QY 363 GAAATAGGAGGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 422  
 Db GAAATAGGAGGGGCTTCGGTGTACGGGCTTACGGGCTTACGGGCTTACGGGCTTACGGGCTT 703

QY 423 GACGAAACCACTAAATTCGGATTCGACATATTCGATATTCGATATTCGATATTCGATATTC 482  
 Db GACGAAACCACTAAATTCGGATTCGACATATTCGATATTCGATATTCGATATTCGATATTC 763

QY 483 ATAAAGCCATTGACCATTCACCATTTGGTGCACCTC 523  
AAC89169  
Db 764 ATAAAGCCATTGACCATTCACCATTTGGTGCACCTC 804

RESULT 45  
ID AAC89169 standard; DNA; 3885 BP.

XX AAC89169;  
XX 08-MAR-2001 (first entry)  
XX

DE AdRSVPHYDE region A coding sequence.

XX p-HYDE; cytostatic; gene therapy; apoptosis; leukaemia; prostate;  
KW tumour suppressor gene; DNA repair; cancer; melanoma; lymphoma;  
KW colorectal; pancreatic; breast; brain; gastric carcinoma; ds.  
XX

XX Unidentified.

XX WO200071564-A2.

XX 30-NOV-2000.

XX 01-MAY-2000; 2000WO-US011456.

XX 29-APR-1999; 99US-00302457.

XX 29-APR-1999; 99US-0131607P.

XX 08-FEB-2000; 2000US-00499817.

XX (UYTE-) UNIV TENNESSEE RES CORP.

XX Steiner MS, Wang C, Rinaldy A, Menon R;

XX WPI; 2001-032016/04.

XX New isolated nucleic acid encoding a mammalian p-Hyde protein of the p-Hyde family is useful for treating cancer, e.g. prostate cancer.

XX Disclosure; Fig 10; 171pp; English.

XX The present sequence is region A of AdRSVPHYDE. AdRSVPHYDE is an adenovirus vector expressing p-HYDE. p-HYDE induces susceptibility of a cancer cell to cell death. The p-HYDE gene is associated with the regression of tumour growth in vivo, the induction to susceptibility to apoptosis caused by UV or chemotherapy induced DNA damage and prevention of DNA repair with the upregulation of apoptosis as the result of UV damage and the failure to repair DNA. The present sequence may be used to treat cancer, preferably melanoma, lymphoma, leukaemia, prostate, colorectal, pancreatic, breast, brain or gastric carcinoma

XX Sequence 3885 BP; 847 A; 1039 C; 1063 G; 936 T; 0 U; 0 Other;

Query Match 75.1%; Score 393; DB 4; Length 3885;  
Best Local Similarity 98.8%; Pred. No. 3.2e-127;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGATGTACGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTTAGGCG 182  
Db 404 GCGCCCGATGTACGGCCAGATATACGGGTATCTGAGGGGACTAGGGTGTTAGGCG 463

QY 183 AAAAGCGGGCTTCGGTTGTACGCGGTAGGAGTCCCTCAGGATATAGTATTCGCTT 242  
Db 464 AAAAGCGGGCTTCGGTTGTACGCGGTAGGAGTCCCTCAGGATATAGTATTCGCTT 523

QY 243 TTGCATAGGAGGGGAAATAGTCTTATGCATATCTTGTAGTCTTGCACATGGTA 302  
Db 524 TTGCATAGGAGGGGAAATAGTCTTATGCATATCTTGTAGTCTTGCACATGGTA 583

QY 303 ACGATGAGTTACGACATGCTTACAGGAGGAGAAAGCAGCGTCATGCCGATTTGGTG 362  
Db 584 ACGATGAGTTACGACATGCTTACAGGAGGAGAAAGCAGCGTCATGCCGATTTGGTG 643

QY 363 GAAGTAAAGTGGTACGATCGTCTTATTAGGAGGCAACAGACGGGTCTGCATGGATT 422  
Db 644 GAAGTAAAGTGGTACGATCGTCTTATTAGGAGGCAACAGACGGGTCTGCATGGATT 703  
QY 423 GGAGAAACCACTAAATTCGGCATTCGAGAGATTTATTTAAGTCCCTAGCTGATACA 482  
Db 704 GGAGAAACCACTAAATTCGGCATTCGAGAGATTTATTTAAGTCCCTAGCTGATACA 763  
QY 483 ATAAAGCCATTGACCATTCACCATTTGGTGCACCTC 523  
Db 764 ATAAAGCCATTGACCATTCACCATTTGGTGCACCTC 804

RESULT 46

AAA09085

ID AAA09085 standard; DNA; 4487 BP.

XX AAA09085;

XX 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 10-AUG-2000 (first entry)

XX

DE AdRSV-beta-galactosidase vector region A.

XX Region A; replication-deficient; vector; lacZ; beta-galactosidase;

XX Rous Sarcoma Virus; RSV; promoter; cytotoxicity; cytostatic; pro-drug;

XX prostate cancer; gene therapy; ss.

XX Human adenovirus type 5.

XX Rous sarcoma virus.

XX Escherichia coli.

XX Chimeric.

XX WO200020038-A1.

XX 13-APR-2000.

XX 01-OCT-1999; 99WO-US020907.

XX 02-OCT-1998; 98US-00165730.

XX (GENO-) GENOTHERAPEUTICS INC.

XX Steiner MS;

XX WPI; 2000-303646/26.

XX Inducing cellular cytotoxicity of tumor cell comprises introducing replication-deficient adenovirus type 5 expression vector containing gene encoding for enzyme having ability to convert nontoxic prodrug into cancer killing drug.

XX Claim 4; Fig 18B; 178pp; English.

XX This sequence comprises Region A of a replication-deficient adenovirus type 5 vector containing a lacZ gene (encoding beta-galactosidase (beta-gal)) under the control of the Rous Sarcoma Virus (RSV) promoter.

XX Inducing cellular cytotoxicity of a tumor cell comprises introducing a replication-deficient adenovirus type 5 expression vector comprising a gene that encodes for an enzyme that has the ability to convert a non-toxic pro-drug into a cancer killing drug which then destroys cancer cells.

XX The adenovirus genome preferably has a deletion in an E1 and E3 region and an insertion within the region of a nucleic acid encoding Escherichia coli beta-gal under the control of a promoter. The pro-drug active site is masked by beta-gal. Functional beta-gal is expressed from the vector so as to activate the pro-drug into an agent toxic to the cells.

XX Beta-gal can be under the control of an RSV, probasin (PB), Prostate Specific Antigen (PSA) or Mouse Mammary Tumor Virus (MMTV) promoter. The vectors provide a novel way to treat prostate cancer by gene therapy. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 15-SEP-2003 to standardise OS field)

XX

XX

XX  
SQ Sequence 4487 BP; 1031 A; 1148 C; 1288 G; 1020 T; 0 U; 0 Other;  
Query Match 75.1%; Score 393; DB 3; Length 4487;  
Best Local Similarity 98.8%; Pred. No. 3.5e-127;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 123 GCTTCGCGATGTAACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
DB 404 GCGCCCGAATGTAACGGGCGAGATATACGGGTATCTGAGGGGACTAGGGTGTGTTAGGCG 463  
QY 183 AAAAGCGGGCTTCGGTGTACGGGTATAGGAGTCCCTCAGGATATAGTATGCTTTCGCTT 242  
DB 464 AAAAGCGGGCTTCGGTGTACGGGTATAGGAGTCCCTCAGGATATAGTATGCTTTCGCTT 523  
QY 243 TTGCTATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGGTA 302  
DB 524 TTGCTATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGGTA 583  
QY 303 ACGATGAGTTAGCAATGCTTACAAAGGAGAGAAAGCAACCGTGCATGCGGATTTGGTG 362  
DB 584 ACGATGAGTTAGCAATGCTTACAAAGGAGAGAAAGCAACCGTGCATGCGGATTTGGTG 643  
QY 363 GAAGTAAGTGTGTAACGCTTATAGGAGGCAACAGACGGGTCTGCATGGATT 422  
DB 644 GAAGTAAGTGTGTAACGCTTATAGGAGGCAACAGACGGGTCTGCATGGATT 703  
QY 423 GGACGACCACTAAATTCGGATTCGAGAGATTTGATTTAAGTGCCTAGCTCGATACA 482  
DB 704 GGACGACCACTAAATTCGGATTCGAGAGATTTGATTTAAGTGCCTAGCTCGATACA 763  
QY 483 ATAAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
DB 764 ATAAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 804

RESULT 47  
AAAS9078  
ID AAAS9078 standard; DNA; 8238 BP.  
AC AAAS9078;  
XX 07-NOV-2000 (first entry)  
DT Nucleotide sequence of a plasmid.  
DE Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;  
KW ss.  
KW Synthetic.  
OS WO20042208-A1.  
PN 20-JUL-2000.  
PD 14-JAN-2000; 2000WO-EP000265.  
PF 14-JAN-1999; 99US-0115920P.  
PR (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
FA (SRI ) SCRIPPS RES INST.  
XX Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;  
PI Skripchenko Y;  
XX WFI; 2000-476068/41.  
DR New nucleic acid comprising an adenovirus tripartite leader nucleotide  
XX for producing high-capacity and targeted vectors for adenovirus-based  
XX gene therapy.  
XX Disclosure; Page 195-198; 212pp; English.  
PS

XX The specification describes a nucleic acid molecule comprising an  
CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence  
CC comprising two different TPL exons or three same or different TPL exons.  
CC The nucleic acid is used to produce an adenovirus vector particle,  
CC deliver an exogenous gene to a target cell, pseudotype recombinant viral  
CC vectors, target an adenovirus vector to a cell, produce a modified  
CC adenovirus, deliver a heterologous gene to an animal and produce a  
CC gutless adenoviral vector particle. The present sequence represents a  
CC plasmid, which is used in the course of the invention  
XX  
SQ Sequence 8238 BP; 1762 A; 2156 C; 2340 G; 1980 T; 0 U; 0 Other;  
Query Match 75.1%; Score 393; DB 3; Length 8238;  
Best Local Similarity 98.8%; Pred. No. 4.7e-127;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 123 GCTTCGCGATGTAACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
DB 404 GCGCCCGAATGTAACGGGCGAGATATACGGGTATCTGAGGGGACTAGGGTGTGTTAGGCG 463  
QY 183 AAAAGCGGGCTTCGGTGTACGGGTATAGGAGTCCCTCAGGATATAGTATGCTTTCGCTT 242  
DB 464 AAAAGCGGGCTTCGGTGTACGGGTATAGGAGTCCCTCAGGATATAGTATGCTTTCGCTT 523  
QY 243 TTGCTATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGGTA 302  
DB 524 TTGCTATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGGTA 583  
QY 303 ACGATGAGTTAGCAATGCTTACAAAGGAGAGAAAGCAACCGTGCATGCGGATTTGGTG 362  
DB 584 ACGATGAGTTAGCAATGCTTACAAAGGAGAGAAAGCAACCGTGCATGCGGATTTGGTG 643  
QY 363 GAAGTAAGTGTGTAACGCTTATAGGAGGCAACAGACGGGTCTGCATGGATT 422  
DB 644 GAAGTAAGTGTGTAACGCTTATAGGAGGCAACAGACGGGTCTGCATGGATT 703  
QY 423 GGACGACCACTAAATTCGGATTCGAGAGATTTGATTTAAGTGCCTAGCTCGATACA 482  
DB 704 GGACGACCACTAAATTCGGATTCGAGAGATTTGATTTAAGTGCCTAGCTCGATACA 763  
QY 483 ATAAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
DB 764 ATAAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 804

RESULT 48  
AAL56867  
ID AAL56867 standard; DNA; 33622 BP.  
AC AAL56867;  
XX 06-NOV-2003 (first entry)  
DT DNA sequence of the recombinant adenoviral Av3nBg vector.  
DE Fibre shaft modification; adenoviral vector; cell entry pathway; penton;  
XX CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;  
KW gene therapy; fibre knob; Av3nBg; ds.  
XX Human adenovirus type 5.  
OS Unidentified.  
XX WO2003062400-A2.  
PN 31-JUL-2003.  
PD 24-JAN-2003; 2003WO-US002295.  
PF 24-JAN-2002; 2002US-0350388P.  
PR 26-JUN-2002; 2002US-0391967P.  
XX (SRI ) SCRIPPS RES INST.  
PA

PA (NOVS ) NOVARTIS AG.  
 XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;  
 PI WPI; 2003-627459/59.  
 DR New modified adenovirus capsid protein, useful as a base vector for  
 PT producing redirected adenoviruses.  
 XX Example 1; Page 156-165; 132pp; English.  
 XX This invention relates to novel fibre shaft modifications in adenoviral  
 CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a  
 CC specific targeted tissue or organ, accordingly gene therapy requires the  
 CC ablation of normal virus tropism. If successful, systemic vector delivery  
 CC into a peripheral vein would be targeted to the desired location in the  
 CC body without any associated side effects, which would permit lower, less  
 CC toxic vector doses that are also potentially less immunogenic. The  
 CC present invention describes capsid modifications, specifically fibre  
 CC shaft mutations that when expressed on adenoviral particles ablates  
 CC binding to heparin sulphate proteoglycans (HSP) thus providing detargeted  
 CC vectors. Furthermore, when this is combined with modifications of other  
 CC adenoviral proteins involved in the cell entry pathway such as the fibre  
 CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors  
 CC become fully detargeted. As such, these fully ablated particles can be  
 CC used in vivo as base vectors for producing redirected adenoviruses with  
 CC the desired cell specificity. This polynucleotide sequence is the  
 CC recombinant E1, E2a and E3-deleted adenoviral vector (Avn99) that  
 CC encodes a nuclear localising beta-galactosidase, used in the  
 CC exemplification of the invention  
 XX  
 XX Sequence 33622 BP; 7857 A; 9539 C; 9277 G; 6949 T; 0 U; 0 Other;

Query Match 75.1%; Score 393; DB 8; Length 33622;  
 Best Local Similarity 98.8%; Pred. No. 9.8e-127;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 123 GCTTCGCATGTACGGCCAGATATTCCGCTATCTGAGGGACTAGGCTGTGTTAGGCG 182  
 Db 396 GCCTCCCGATGTACGGCCAGATATTACCGGTATCTGAGGGACTAGGCTGTGTTAGGCG 455  
 QY 183 AAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
 Db 456 AAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 515  
 QY 243 TTCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 302  
 Db 516 TTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 575  
 QY 303 ACATGAGTTAGCAATGCTTTACAGGAGAGAAAACACCGTGCATGCCATTTGGTG 362  
 Db 576 ACATGAGTTAGCAATGCTTTACAGGAGAGAAAACACCGTGCATGCCATTTGGTG 635  
 QY 363 GAAGTAAGTGTGTACGATCGTGCCTTTATAGGAAGGCAACAGCGGCTTGCATGAT 422  
 Db 636 GAAGTAAGTGTGTACGATCGTGCCTTTATAGGAAGGCAACAGCGGCTTGCATGAT 695  
 QY 423 GGACGACCACTTAATTCGCATTCGAGATATTTGATTAAGTGCCTAGCTGATACA 482  
 Db 696 GGACGACCACTTAATTCGCATTCGAGATATTTGATTAAGTGCCTAGCTGATACA 755  
 QY 483 ATAAAGCCATTTGACCATTTTACCATTTGATTTGTTGTTGTTGTTGTTGTTGTT 523  
 Db 756 ATAAAGCCATTTGACCATTTTACCATTTGATTTGTTGTTGTTGTTGTTGTTGTT 796  
 RESULT 49  
 AAZ94163  
 ID AAZ94163 standard; DNA; 34302 BP.  
 XX  
 AC AAZ94163;  
 XX  
 DT 15-SEP-2003 (revised)

DT 19-JUN-2000 (first entry)  
 XX Adenovirus vector AdRSVP16 used for prostate cancer gene therapy.  
 DE AdRSVP16; adenovirus; vector; RSV; promoter; human; p16;  
 XX tumour suppressor gene; prostate cancer; gene therapy; ds.  
 KW Human adenovirus type 5.  
 XX Rous sarcoma virus.  
 OS Homo sapiens.  
 OS Chimeric.  
 OS  
 PH Key Location/Qualifiers  
 FT promoter 410..805  
 FT /tag= a  
 FT misc\_feature 1055..2014  
 FT /tag= b  
 FT /note= "p16 sense cDNA"  
 XX WO200014211-A1.  
 PN 16-MAR-2000.  
 XX  
 PD 02-SEP-1999; 99WO-US018833.  
 XX 02-SEP-1998; 98US-00145729.  
 PR (GENO-) GENOTHERAPEUTICS INC.  
 XX Steiner MS, Lu Y;  
 PI WPI; 2000-256967/22.  
 XX  
 DR Replication-deficient adenovirus type 5 expression vector, useful in gene  
 PT therapy of prostate cancer, comprises a nucleic acid encoding p16 under  
 PT the control of a Rous Sarcoma virus promoter.  
 XX  
 PS Disclosure; Fig 13; 118pp; English.  
 XX  
 CC The present sequence is that of replication-deficient adenovirus vector  
 CC AdRSVP16, deposited as ATCC VR 2626. The vector is a type 5 adenovirus  
 CC in which the E1 and E3 regions of the genome have been removed, and a p16  
 CC tumour suppressor gene (see AAZ94162) has been inserted under control of  
 CC a Rous sarcoma virus (RSV) promoter (see AAZ94161). AdRSVP16 can be used  
 CC in the gene therapy of prostate cancer to replace a missing, mutated or  
 CC inactivated p16 gene. In vitro, PC3 cells which were stably transfected  
 CC with the vector showed a 70% reduction in cell number. The vector also  
 CC inhibited growth of prostate cancer cells PPC-1, DU145 and PC3 in  
 CC culture. PPC-1 tumours grown in nude mice treated by a single injection  
 CC of AdRSVP16 had a marked reduction in tumour size when compared to  
 CC untreated control. The mice also survived for longer. Transduction rates  
 CC were over 90%, with transgene expression detectable in tumours for up to  
 CC 2 wk. (Updated on 15-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 34302 BP; 7995 A; 9797 C; 9303 G; 7207 T; 0 U; 0 Other;  
 Query Match 75.1%; Score 393; DB 3; Length 34302;  
 Best Local Similarity 98.8%; Pred. No. 9.9e-127;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 123 GCTTCGCATGTACGGCCAGATATTCCGCTATCTGAGGGACTAGGCTGTGTTAGGCG 182  
 Db 404 GCCTCCCGATGTACGGCCAGATATTACCGGTATCTGAGGGACTAGGCTGTGTTAGGCG 463  
 QY 183 AAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
 Db 464 AAAAGCGGGCTTCGGTTGTACCGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 523  
 QY 243 TTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 302  
 Db 524 TTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGTA 583  
 QY 303 ACATGAGTTAGCAATGCTTTACAGGAGAGAAAACACCGTGCATGCCATTTGGTG 362





FT mat\_peptide /note= "Splice donor site"  
 FT 909..1094  
 FT /tag= g  
 FT /label= gag\_p10\_peptide  
 FT 1095..11814  
 FT /tag= h  
 FT /label= gag\_p27\_peptide  
 FT 1843..2108  
 FT /tag= i  
 FT /label= gag\_p12\_peptide  
 FT 2109..2480  
 FT /tag= j  
 FT /label= gag\_p15\_peptide  
 FT 2501..5189  
 FT /tag= k  
 FT /product= "Reverse transcriptase polymerase (pol)"  
 FT 2501..4216  
 FT /tag= l  
 FT /label= Polymerase\_pol\_RT  
 FT 4217..5186  
 FT /tag= m  
 FT /label= Polymerase\_pol\_IN  
 FT 5075..5078  
 FT /tag= n  
 FT /note= "env splice acceptor site"  
 FT 5245..6882  
 FT /tag= o  
 FT /product= "Envelope protein (env)"  
 FT 5245..6264  
 FT /tag= p  
 FT /label= env\_gp85\_peptide  
 FT 6265..6879  
 FT /tag= q  
 FT /label= env\_gp37\_peptide  
 FT 6983..6986  
 FT /tag= r  
 FT /note= "Clal splice acceptor site"  
 FT 7154..7165  
 FT /tag= s  
 FT /label= PPT  
 FT 7166..7494  
 FT /tag= t  
 FT /label= 7394  
 FT /tag= u  
 FT /note= "3'end unique sequence"  
 FT 7395..7415  
 FT /tag= v  
 FT /rpt\_type= DIRECT  
 FT 7416..7494  
 FT /tag= w  
 FT /note= "5'end unique sequence"  
 FT 7649..11258  
 FT /tag= x  
 FT /label= pBR322\_vector  
 FT 11394..11623  
 FT /tag= y  
 FT /note= "3'end unique sequence"  
 FT 7649..11258  
 FT 02-DEC-1999.  
 FT 28-MAY-1999; 99MO-US011780.  
 FT 29-MAY-1998; 98US-0087220P.  
 FT (SCRI ) SCRIPPS RES INST.  
 FT Cheresch DA, Eliceiri B, Schwartzberg PL;  
 FT WPI; 2000-116335/10.  
 FT Using tyrosine kinase Src for modulating angiogenesis in tissues useful

PT in, e.g. treatment of chronic articular rheumatism.  
 XX Claim 15; Page 59-66; 80pp; English.  
 CC The present DNA sequence is the viral expression vector, RCASBP(A)  
 CC construct. This vector is based on a replication competent avian sarcoma  
 CC virus with an enhanced Bryan polymerase (BP) and is specific for the 'A'  
 CC type envelope glycoprotein expressed on normal avian cells. The vector  
 CC expresses Src protein or modified Src, that can be used to modulate  
 CC angiogenesis. When the Src protein is inactivated, angiogenesis is  
 CC inhibited, while when it is activated, angiogenesis is potentiated. This  
 CC modified or mutant Src can be used to treat inflammatory diseases like,  
 CC arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis,  
 CC osteoporosis and cancer associated disorders  
 XX  
 SQ Sequence 11627 BP; 2796 A; 2808 C; 3324 G; 2699 T; 0 U; 0 Other;  
 Query Match 74.6%; Score 390.2; DB 3; Length 11627;  
 Best Local Similarity 99.2%; Pred. No. 5.5e-126;  
 Matches 392; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 128 GCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGGTGTGTAGGCGAAG 187  
 DB 7034 GCGATGTACGGGCCAGATATACGGGTATCTGAGGGGACTAGGGGTGTGTAGGCGAAG 7093  
 QY 188 CGGGGCTTCGGTGTACGGGTGTAGGAGTCCCTCAGGATATAGTATTCGCTTTTGA 247  
 DB 7094 CGGGGCTTCGGTGTACGGGTGTAGGAGTCCCTCAGGATATAGTATTCGCTTTTGA 7153  
 QY 248 TAGGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGAT 307  
 DB 7154 TAGGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGAT 7213  
 QY 308 GAGTTAGCAATGCTTACAGGAGAGAGAAAAGCACCGTGCATGCCGATTGCTGGAAGT 367  
 DB 7214 GAGTTAGCAATGCTTACAGGAGAGAGAAAAGCACCGTGCATGCCGATTGCTGGAAGT 7273  
 QY 368 AAGGTGTACGATCGTGCCTTTATTAGGAAGGCAACAGACGGGTCTGACATGATTTGAACG 427  
 DB 7274 AAGGTGTACGATCGTGCCTTTATTAGGAAGGCAACAGACGGGTCTGACATGATTTGAACG 7333  
 QY 428 AACCACTTAATTCGGCATTCGAGAGATATTGATTTAAGTGCCTAGCTCGATACATAAA 487  
 DB 7334 AACCACTTAATTCGGCATTCGAGAGATATTGATTTAAGTGCCTAGCTCGATACATAAA 7393  
 QY 488 CGCCATTGTGACCATTCACCAATTTGGTGTGCACCT 522  
 DB 7394 CGCCATTGTGACCATTCACCAATTTGGTGTGCACCT 7428  
 RESULT 52  
 AAL55269  
 ID AAL55269 standard; DNA; 16958 BP.  
 XX  
 AC AAL55269;  
 XX  
 DT 10-MAY-2003 (first entry)  
 XX  
 DE DNA of expression vector RC77, SEQ ID No 3.  
 XX  
 KW Vector; excisable; site-specific recombinase; enzyme; exogenous;  
 KW signalling molecule; transcription factor; cell metabolism;  
 KW differentiation state; kinase; phosphatase; ds.  
 OS Unidentified.  
 XX  
 FN WO2003002735-A2.  
 XX  
 PD 09-JAN-2003.  
 XX  
 PF 28-JUN-2002; 2002WO-CA000997.  
 XX  
 PR 28-JUN-2001; 2001US-0301149P.

XX (PHEN-) PHENOGENE THERAPEUTICS INC.  
 XX Lanctot C, Gingras R, Gaumont M;  
 XX WPI; 2003-210275/20.  
 XX New vector having a nucleic acid sequence excisable by site-specific  
 PT recombination, useful for identifying or selecting exogenous nucleic  
 PT acids with desired features, e.g. nucleic acids encoding transcription  
 PT factors or kinases.  
 XX Claim 24; Page 103-112; 122pp; English.  
 XX The invention relates to novel vectors comprising nucleic acid sequences  
 CC excisable by a site-specific recombinase. The vectors or cells are useful  
 CC for identifying or selecting an exogenous nucleic acid having a desired  
 CC feature, e.g. nucleic acids encoding signalling molecules, transcription  
 CC factors or other proteins involved in changes of cell metabolism or  
 CC differentiation state (e.g. kinase or phosphatase). This polynucleotide  
 CC sequence represents the DNA of the vector RC77 relating to the invention  
 XX Sequence 16958 BP; 4816 A; 4210 C; 4125 G; 3807 T; 0 U; 0 Other;  
 SQ  
 Query Match 72.5%; Score 379; DB 7; Length 16958;  
 Best Local Similarity 98.5%; Pred. No. 6e-122;  
 Matches 393; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
 QY 126 TCGCGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGHGTGTTAGCGGAAA 185  
 Db 14374 TAGCGATGTACGGGCCAGATATACGGGTATCTGAGGGGACTAGGGGTGTGTTAGCGGAAA 14433  
 QY 186 AGCGGGCTTCGGTGTACGGGTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTG 245  
 Db 14434 AGCGGGCTTCGGTGTACGGGTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTG 14493  
 QY 246 CATAGGAGGGGAAAATAGTCTTATGCAATACACTTTGTAGTCTTTCGCAACATGTTAACG 305  
 Db 14494 CATAGGAGGGGAAAATAGTCTTATGCAATACACTTTGTAGTCTTTCGCAACATGTTAACG 14553  
 QY 306 ATGAGTTAGCAATGCTTACAGGAGAGAAAAGACCGTCGATCGGTTGGTGGAA 365  
 Db 14554 ATGAGTTAGCAATGCTTACAGGAGAGAAAAGACCGTCGATCGGTTGGTGGAA 14613  
 QY 366 GTAAGGTGTAGCATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGCAATTGGA 425  
 Db 14614 GTAAGGTGTAGCATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGCAATTGGA 14673  
 QY 426 CGAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAT 484  
 Db 14674 CGAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAT 14733  
 QY 485 AAACGCCATTGACCAATTCACCAATGTTGTGACCTC 523  
 Db 14734 AAACGCCATTGACCAATTCACCAATGTTGTGACCTC 14772  
 RESULT 53  
 AAZ94161  
 ID AAZ94161 standard; DNA; 397 BP.  
 XX AAZ94161;  
 XX 19-JUN-2000 (first entry)  
 XX 395 Nucleic acid Rous sarcoma virus promoter.  
 DE Adenovirus; vector; RSV; promoter; prostate cancer; gene therapy;  
 KW tumour suppressor gene; p16; ss.  
 XX Rous sarcoma virus.  
 OS  
 PN WO200014211-A1.

XX 16-MAR-2000.  
 PD 02-SEP-1999; 99WO-US018833.  
 XX 02-SEP-1998; 98US-00145729.  
 XX (GENO-) GENOTHERAPEUTICS INC.  
 XX Steiner MS, Lu Y;  
 XX WPI; 2000-256967/22.  
 XX Replication-deficient adenovirus type 5 expression vector, useful in gene  
 PT therapy of prostate cancer, comprises a nucleic acid encoding p16 under  
 PT the control of a Rous Sarcoma virus promoter.  
 XX Claim 1; Page 12; 118pp; English.  
 CC The present sequence is that of 395 nucleic acid Rous sarcoma virus (RSV)  
 CC promoter. A novel replication-deficient adenovirus type 5 expression  
 CC vector of the invention, termed AdRSVp16 (see AAZ94161), has a deletion  
 CC in an E1 and E3 region of the genome and contains a p16 tumour suppressor  
 CC gene under the control of the RSV promoter. The adenoviral vector is used  
 CC in the gene therapy of prostate cancer, in which p16 is frequently  
 CC inactivated. Gene therapy is used to replace a missing, mutated or  
 CC and/or progression of the tumour  
 XX Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;  
 SQ  
 Query Match 71.6%; Score 374.4; DB 3; Length 397;  
 Best Local Similarity 98.2%; Pred. No. 3.6e-121;  
 Matches 389; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
 QY 129 CGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGGTGTGTTAGCGGAAAAGC 188  
 Db 1 CGATGTACGGGCCAGATATACGGGTATCTGAGGGGACTAGGGGTGTGTTAGCGGAAAAGC 60  
 QY 189 GGGGCTTCGGTGTACGGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCAT 248  
 Db 61 GGGGCTTCGGTGTACGGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCAT 120  
 QY 249 AGGAGAGGGGAAAATAGTCTTATGCAATACACTTTGTAGTCTTTCGCAACATGTTAACGATG 308  
 Db 121 AGCCAGGGGAAAATAGTCTTATGCAATACACTTTGTAGTCTTTCGCAACATGTTAACGATG 180  
 QY 309 AGTTAGCAACATGCTTACAGGAGAGAAAAGACCGTCGATCGGATTCGTTGGAAGTA 368  
 Db 181 AGTTAGCAACATGCTTACAGGAGAGAAAAGACCGTCGATCGGATTCGTTGGAAGTA 240  
 QY 369 AGGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGAATGGAAGA 428  
 Db 241 AGGTGTACGATCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGAATGGAAGA 300  
 QY 429 ACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAATAA 487  
 Db 301 ACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAATAA 360  
 QY 488 CGCCATTGACCAATTCACCAATGTTGTGACCTC 523  
 Db 361 CGCCATTGACCAATTCACCAATGTTGTGACCTC 396  
 RESULT 54  
 AAA14719  
 ID AAA14719 standard; DNA; 397 BP.  
 XX AAA14719;  
 XX 08-AUG-2000 (first entry)  
 XX Nucleotide sequence of the Rous Sarcoma virus promoter.

XX Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;  
 KW replication-deficient adenovirus type 5; suicide gene therapy;  
 KW cancer cell; chemotherapy; beta-lactamase prodrug enzyme; prodrug TCM;  
 KW anticancer; tumor; leukemia; breast cancer; Wilms tumor;  
 KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;  
 KW papillary adenocarcinoma; promoter; ss.  
 XX Rous sarcoma virus.  
 OS Rous sarcoma virus.  
 XX WO200020608-A1.  
 PN 13-APR-2000.  
 XX 01-OCT-1999; 99WO-US020908.  
 XX 02-OCT-1998; 98US-00165321.  
 PR (GENO-) GENOTHERAPEUTICS INC.  
 PA Steiner MS;  
 XX WPI; 2000-303788/26.  
 DR Treating cancer using viral vectors which encode enzymes that convert  
 PT inactive drugs to active cytotoxic agents, expression of the enzyme is  
 PT tissue specific therefore targeting the effects of the drug to tumor  
 PT cells.  
 XX Disclosure; Page 13-14; 130pp; English.  
 XX The specification describes a method for inducing cellular cytotoxicity  
 CC in tumor cells using replication-deficient adenovirus type 5 expression  
 CC vectors. The vectors comprise a sequence encoding a beta-lactamase under  
 CC the control of a Rous sarcoma virus in combination with a prodrug  
 CC conjugated to a toxic agent. Tissue specific expression of the enzyme  
 CC converts the inactive drugs into active cancer killing agents. The  
 CC adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-  
 CC lactamase sequence is inserted within this region. The vectors are used  
 CC for suicide gene therapy. This involves introducing genes into cancer  
 CC cells that encode enzymes capable of converting inactive drugs into  
 CC active cancer killing agents. If tissue specific promoters are coupled to  
 CC the prodrug enzymes, then production of the prodrug will be tissue  
 CC specific and targeted to the tumor. Therefore the cancer cells act as  
 CC their own factories to activate chemotherapy agents and commit suicide.  
 CC Beta-lactamase prodrug enzymes convert prodrug TCM into an active  
 CC anticancer agent which is cytotoxic to cancer cells PPC-1. The method is  
 CC used to treat patients with cancers of the brain, bladder or prostate. It  
 CC may also be used to treat a range of other tumors such as leukemia,  
 CC breast cancer, Wilms tumor, small cell lung carcinoma, Ewing's sarcoma,  
 CC colon carcinoma and papillary adenocarcinomas. The present sequence  
 CC represents the Rous Sarcoma virus promoter, which was used to  
 CC construct vectors of the invention  
 XX Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;  
 SQ Query Match 71.6%; Score 374.4; DB 3; Length 397;  
 Best Local Similarity 98.2%; Pred. No. 3.6e-121;  
 Matches 389; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
 QY 129 CGATGACGGGCGCATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGGGGAAAGC 188  
 DB 1 CGATGTACGGGCGCATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGGGGAAAGC 60  
 QY 189 GGGGCTTCGGTGTACGGGTAGGAGTCCCTCAGCATATAGTTCGCTTTTGCAAT 248  
 DB 61 GGGGCTTCGGTGTACGGGTAGGAGTCCCTCAGCATATAGTTCGCTTTTGCAAT 120  
 QY 249 AGGAGGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGTAACGATG 308  
 DB 121 AGCCAGGGGGAAATAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGTAACGATG 180  
 QY 309 AGTTAGCAATCGCTTACAGGAGAGAAAAGCACCGTGCATGCGGATTCGTTGGGAAGTA 368

DB 181 AGTTAGCAATCGCTTACAGGAGAGAAAAGCACCGTGCATGCGGATTCGTTGGGAAGTA 240  
 QY 369 AGGTGGTACGATCGTCCCTTATTAGGAAGGCAACAGAGGGTCTGACATGATTGGACGA 428  
 DB 241 AGGTGGTACGATCGTCCCTTATTAGGAAGGCAACAGAGGGTCTGACATGATTGGACGA 300  
 QY 429 ACCACTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCCCTAGCTCGATCAATAAAA 487  
 DB 301 ACCACTAAATTCGGCATTCGACAGAT-ATTGTATTAAAGTGCCCTAGCTCGATCAATAAAA 360  
 QY 488 CGCCATTGACCATTCACCATTCGATGGTGGACCTC 523  
 DB 361 CGCCATTGACCATTCACCATTCGATGGTGGACCTC 396  
 RESULT 55  
 AAZ93077  
 ID AAZ93077 standard; DNA; 397 BP.  
 AC AAZ93077;  
 XX 04-JUL-2000 (first entry)  
 DE Rous Sarcoma Virus promoter sequence.  
 DE Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;  
 XX Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;  
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.  
 XX Rous sarcoma virus.  
 OS Rous sarcoma virus.  
 XX WO200014256-A1.  
 PN 16-MAR-2000.  
 PD 03-SEP-1999; 99WO-US018834.  
 PP 04-SEP-1998; 98US-00148275.  
 PR (GENO-) GENOTHERAPEUTICS INC.  
 PA Steiner MS, Lu Y;  
 XX WPI; 2000-257001/22.  
 PT Replication-deficient adenovirus type 5 expression vectors used for gene  
 PT therapy of cancer, especially prostate cancer, comprising an insertion of  
 PT nucleic acid encoding cytochrome p450 genes.  
 XX Claim 8; Page 18; 110pp; English.  
 CC Replication-deficient adenovirus type 5 expression vectors comprise an  
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome  
 CC and an insertion within the region under the control of a Rous Sarcoma  
 CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three  
 CC such expression vectors are described, the inserted nucleic acids in each  
 CC being the following: Vector (I) has an insertion of a nucleic acid  
 CC encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-  
 CC 2828). Vector (II) has an insertion of a nucleic acid encoding a  
 CC cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector  
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine  
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is  
 CC designated AdRSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell  
 CC can be induced by administering (I) and (III) or (II) into the cell  
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell  
 CC to a prodrug and then administering the prodrug which kills the cell,  
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug  
 CC therapy to transfer a drug susceptibility gene to the tumor which  
 CC activates a nontoxic prodrug intratumorally so the released drug can kill  
 CC the tumor cells containing the drug susceptibility gene  
 XX Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;  
 SQ

Query Match 71.6%; Score 374.4; DB 3; Length 397;  
 Best Local Similarity 98.2%; Pred. No. 3.6e-121;  
 Matches 389; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 129 CGATGTACGGGCGCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTTAGGCGAAAGC 188  
 DB 1 CGATGTACGGGCGCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTTAGGCGAAAGC 60

QY 189 GGGCTTCGGTGTGTCAGGGTATAGGAGTCCCTCAGATATAGTATGCTTTCGTTTGCAT 248  
 DB 61 GGGCTTCGGTGTGTCAGGGTATAGGAGTCCCTCAGATATAGTATGCTTTCGTTTGCAT 120

QY 249 AGGAGCGGGGAATGTAGTCTTATGCAATCTGTAGTCTGCAATGCAATGCAATG 308  
 DB 121 AGGAGCGGGGAATGTAGTCTTATGCAATCTGTAGTCTGCAATGCAATGCAATG 180

QY 309 AGTTAGCAACATGCCCTTACAGGAGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTA 368  
 DB 181 AGTTAGCAACATGCCCTTACAGGAGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTA 240

QY 369 AGGTGTGATGATGTCCTTATAGGAGGCAAGAGCGGTCTGACATGATTTGGACGA 428  
 DB 241 AGGTGTGATGATGTCCTTATAGGAGGCAAGAGCGGTCTGACATGATTTGGACGA 300

QY 429 ACCACTAAATTCGGCATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAA 487  
 DB 301 ACCACTAAATTCGGCATTCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAA 360

QY 488 CGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 DB 361 CGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 396

RESULT 56  
 AAX02780  
 ID AAX02780 standard; DNA; 37808 BP.  
 AC AAX02780;  
 XX  
 XX  
 DT 14-MAY-1999 (first entry)  
 DE Vector pMX-BG DNA.  
 XX  
 XX  
 KW Vector pMX-BG; cloning; adenoviral minimal virus; AdMV; ITR; plasmid;  
 KW inverted terminal repeats; ITR; packaging signal; PSI; bacteriophage;  
 KW virus bank; genomic analysis; transgenic animal; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9902647-A2.  
 XX  
 PD 21-JAN-1999.  
 XX  
 XX  
 PF 06-JUL-1998; 98WO-DB001940.  
 XX  
 PR 10-JUL-1997; 97DE-01029571.  
 PR 10-OCT-1997; 97DE-01044768.  
 XX  
 XX (HEPA-) HEPAVEC GENTHERAPIE AG.  
 XX  
 XX Hillgenberg M, Loeser P, Schnieders F, Sandig V, Strauss M;  
 XX WPI; 1999-120851/10.  
 XX  
 XX New cloning vector for producing adenoviral minimal viruses - useful for  
 PT gene therapy or for preparation of virus banks and transgenic animals.  
 XX  
 XX Disclosure; Page 16-41, 57pp; German.  
 XX  
 XX This invention describes a novel cloning vector (A) for production of  
 CC adenoviral minimal viruses (AdMV). The vector is composed of two  
 CC adenoviral inverted terminal repeats (ITR) and a bacterial plasmid

CC backbone that includes an origin of replication (ori) and bacterial  
 CC resistance gene, in which a packaging signal (PSI) for a bacteriophage is  
 CC cloned. ITR are flanked by two cleavage sites for a restriction  
 CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a  
 CC multiple cloning site for insertion of a therapeutic DNA (in which  
 CC optionally additional, non-coding chromosomal mammalian DNA is cloned),  
 CC optionally a recognition site for a recombinase (between the ITR and PS2)  
 CC and optionally a reporter gene cassette (RGS). AdMV produced from this  
 CC vector are useful for all adenoviral gene transfer applications, for  
 CC production of virus banks (e.g. for genomic analysis) and for preparation  
 CC of transgenic animals. AdMV are safe, compatible with all helper systems,  
 CC and can accommodate large DNA inserts (particularly complete genes with  
 CC the native chromosomal organisation, including the native promoter so  
 CC that problems of over-expression caused by viral promoters are avoided).  
 CC The use of PSI makes possible the use of very efficient and size  
 CC selecting cosmid cloning techniques. When used for transgenic animal  
 CC production, the AdMV can include long homologous regions to provide a  
 CC higher frequency of recombination

XX  
 SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;  
 Query Match 71.3%; Score 372.8; DB 2; Length 37808;  
 Best Local Similarity 98.0%; Pred. No. 1.4e-113;  
 Matches 388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 129 CGATGTACGGGCGCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTTAGCGAAAAGC 188  
 DB 28017 CGATGTACGGGCGCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTTAGCGCCCAGC 28076

QY 189 GGGGCTTCGGTGTGTCAGCGGTAGGAGTCCCTCAGGATATAGTATGCTTTCGTTTGCAT 248  
 DB 28077 GGGGCTTCGGTGTGTCAGCGGTAGGAGTCCCTCAGGATATAGTATGCTTTCGTTTGCAT 28136

QY 249 AGGAGGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGTAACGATG 308  
 DB 28137 AGGAGGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGTAACGATG 28196

QY 309 AGTTAGCAACATGCCCTTACAGGAGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTA 368  
 DB 28197 AGTTAGCAACATGCCCTTACAGGAGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTA 28256

QY 369 AGGTGTGATGATGTCCTTATAGGAGGCAAGAGCGGTCTGACATGATTTGGACGA 428  
 DB 28257 AGGTGTGATGATGTCCTTATAGGAGGCAAGAGCGGTCTGACATGATTTGGACGA 28316

QY 429 ACCACTAAATTCGGCATTCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAA 487  
 DB 28317 ACCACTAAATTCGGCATTCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAA 28376

QY 488 CGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 DB 28377 CGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 28412

RESULT 57  
 AAZ09997  
 ID AAZ09997 standard; cDNA; 5177 BP.  
 XX  
 AC AAZ09997;  
 XX  
 DT 03-DEC-1999 (first entry)  
 XX  
 XX Bovine scavenger receptor class A (ScR)/avidin fusion protein cDNA.  
 DE  
 XX  
 XX Scavenger receptor class A; ScR; avidin; fusion protein; bovine; ECD;  
 KW membrane-spanning domain; extracellular domain; biotin-binding activity;  
 KW endocytosis; ss.  
 XX  
 OS Synthetic.  
 OS Bos taurus.  
 XX  
 XX Key Location/Qualifiers  
 PH 1071..2269  
 FT CDS

```

FT      /tag= a
FT      /product= "ScR/avidin fusion protein"
XX
XX      WO9942577-A2.
XX
XX      26-AUG-1999.
XX
XX      23-FEB-1999; 99WO-GB000546.
XX
XX      23-FEB-1998; 98GB-00003757.
XX
XX      24-JUN-1998; 98GB-00013653.
XX
XX      (EURO-) EUROGENE LTD.
XX
XX      Yla-Herttuala S, Kulomaa M, Lehtolainen P, Marjomaki V, Airenne K;
XX
XX      WPI; 1999-561345/47.
XX
XX      P-PSDB; AAY03098.
XX
XX      New fusion proteins having an extracellular domain with biotin-binding
XX      PT activity, used to target biotinylated molecules to specific sites in
XX      PT tissues.
XX
XX      Disclosure; Page 15-21; 23pp; English.
XX
XX      This invention describes a novel protein (A) which comprises a membrane-
XX      CC spanning domain and an extracellular domain (ECD), where the ECD
XX      CC comprises biotin-binding activity. Using the proteins or encoding nucleic
XX      CC acid molecules it is possible to target biotinylated molecules to
XX      CC specific sites in tissues. Molecules targeted in this way may be taken up
XX      CC by the tissues or cells by endocytosis, allowing the molecules to exert
XX      CC their effects within or on the cell. This sequence encodes a bovine
XX      CC scavenger receptor class A/avidin fusion protein which is used in the
XX      CC description of the invention
XX
XX      Sequence 5177 BP; 1356 A; 1222 C; 1390 G; 1209 T; 0 U; 0 Other;
XX
XX      Query Match      58.0%; Score 303.2; DB 2; Length 5177;
XX      Best Local Similarity 99.0%; Pred. No. 1.7e-95;
XX      Matches 305; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX      QY      216  TCCCTCAGGATAGTAGTTTCGCTTTGCATAGGAGGGGAAATGATCTTATGCA 275
XX      Db      |||||
XX      3062  TCCCTCAGGATAGTAGTTTCGCTTTGCATAGGAGGGGAAATGATCTTATGCA 3121
XX
XX      QY      276  ATACTCTGTAGTCTTGCACATGGTAAAGTATGAGTTAGCAACATGCTTACAGGAGAG 335
XX      Db      |||||
XX      3122  ATACTCTGTAGTCTTGCACATGGTAAAGTATGAGTTAGCAACATGCTTACAGGAGAG 3181
XX
XX      QY      336  AAAAGCACCGTGATCCGATCCGATTCGGAAGTAAAGTGGTACGATCGTGGCTTATTAGGA 395
XX      Db      |||||
XX      3182  AAAAGCACCGTGATCCGATTCGGAAGTAAAGTGGTACGATCGTGGCTTATTAGGA 3241
XX
XX      QY      396  AGCACACAGCGGTCTGACATGGATTGGACGACACCTAAATTCGCGANTGCAGAGATA 455
XX      Db      |||||
XX      3242  AGCACACAGCGGTCTGACATGGATTGGACGACACCTAAATTCGCGANTGCAGAGATA 3301
XX
XX      QY      456  TTGTATTAAAGTGGCTAGCTCGCATCAATAAACGCCATTGACATTACCAATGGTG 515
XX      Db      |||||
XX      3302  TTGTATTAAAGTGGCTAGCTCGCATCAATAAACGCCATTGACATTACCAATGGTG 3361
XX
XX      QY      516  TGCACCTC 523
XX      Db      |||||
XX      3362  TGCACCTC 3369
XX
XX      RESULT 58
XX      AAD28272
XX      ID      AAD28272 standard; DNA; 7170 BP.
XX
XX      AC      AAD28272;
XX
XX      XX      22-APR-2002 (first entry)
XX

```

```

XX      LSRNL vector.
XX
XX      LSRNL vector; pharmaceutical; industrial; diagnostic; screening; MoMuLV;
XX      moloney murine leukemia virus; chimeric; hepatitis B virus; ds.
XX
XX      Hepatitis B virus.
XX
XX      Moloney murine leukemia virus.
XX
XX      Unidentified.
XX
XX      Chimeric.
XX
XX      Key      Location/Qualifiers
XX      LTR      1..589
XX              /tag= a
XX              /note= "MoMuLV 5' LTR"
XX      misc_feature      659..897
XX              /tag= b
XX              /note= "Retroviral packaging region"
XX      misc_feature      1034..1714
XX              /tag= c
XX              /note= "Hepatitis B surface antigen"
XX      promoter      2279..2595
XX              /tag= d
XX              /note= "RSV promoter"
XX      misc_feature      2851..3745
XX              /tag= e
XX              /note= "Neomycin phosphotransferase gene"
XX      LTR      4537..5130
XX              /tag= f
XX              /note= "MoMuLV 3' LTR"
XX
XX      WO200202738-A2.
XX
XX      10-JAN-2002.
XX
XX      29-JUN-2001; 2001WO-US020710.
XX
XX      03-JUL-2000; 2000US-0215925P.
XX      (GALA-) GALA DESIGN INC.
XX
XX      Brenel RD, Miller LU, Bleck GT, York D;
XX
XX      WPI; 2002-154737/20.
XX
XX      Host cell for producing a desired protein and for screening compounds
XX      useful for pharmaceutical, industrial, diagnostic and other purposes,
XX      comprises multiple integrating vectors having an exogenous gene.
XX
XX      Example 1; Fig 12; 191pp; English.
XX
XX      The invention relates to a host cell comprising a genome having at least
XX      two integrated integrating vectors. The integrating vectors comprise at
XX      least one exogenous gene operably linked to a promoter. The host cell is
XX      useful for producing a desired protein and for comparing protein
XX      functions. The host cells comprises a reporter gene which is from gene
XX      fluorescent protein, luciferase, beta-galactosidase and beta-lactamase,
XX      and the assaying step further comprises detecting a signal from the
XX      reporter gene. The desired protein includes proteins for pharmaceutical,
XX      industrial, diagnostic and other purposes. The host cells is useful for
XX      indirectly detecting the expression of a desired protein, comprising
XX      providing the host cell transfected with a vector encoding a
XX      polycistronic sequence comprising a signal protein and a desired protein
XX      operably linked by an internal ribosome entry site (IRES), and culturing
XX      the host cell under suitable conditions so that the signal protein and
XX      the desired protein is produced, where the presence of signal protein
XX      indicates the presence of desired protein. The present sequence is LSRNL
XX      vector used in the invention. The vector comprises the following
XX      elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV viral
XX      packaging signal, hepatitis B surface antigen, RSV promoter, neomycin
XX      phosphotransferase gene and 3' MoMuLV LTR
XX
XX      Sequence 7170 BP; 1688 A; 1891 C; 1841 G; 1750 T; 0 U; 0 Other;
XX

```



Db 2500 GAATTCGGCAATTGCAGAGATAATTGTTATTAAAGTGCTAGCTCGATACAGCAAGCCAT 2559

QY 493 -TTTGACCAATTCACACCAATGGTGCACT 522

Db 2560 TTTTGACCAATTCACCAATGGTGCACT 2590

RESULT 60

AA515665

ID AA515665 standard; DNA; 262 BP.

AC AA515665;

XX 29-JAN-2002 (first entry)

DT Human respiratory syncytial virus promoter.

DE

XX Bcdysone receptor; EcR; ligand binding domain; ds; retinoid X receptor;

KW RXRalpha; DNA-binding domain; RSV promoter; transactivation domain;

KW nuclear receptor; ultraspriacle; gene therapy; protein production;

KW antibody production; high throughput screening; HTS; transgenic plant;

XX transgenic animal.

OS Human respiratory syncytial virus.

XX WO200170816-A2.

PN 27-SEP-2001.

XX

XX 21-MAR-2001; 2001WO-US009050.

PF

XX 22-MAR-2000; 2000US-0191355P.

PR

XX 20-FEB-2001; 2001US-0269799P.

PR

XX (ROHM ) ROHM & HAAS CO.

PA

XX Palli SR, Kapitkaya MZ, Cress DE;

PI WPI; 2001-656841/75.

DR

XX Ecdysone and retinoid X receptor based inducible gene expression systems

PT for use in e.g. gene therapy, large scale production of proteins and cell

PT -based high-throughput screening assays.

XX

XX Example 1; Page 141; 144pp; English.

PS

XX The invention relates to Ecdysone and retinoid X receptor based inducible

CC gene expression systems useful for modulating gene expression in host

CC cells. The gene expression system encodes a polypeptide with a DNA-

CC binding domain recognizes a response element associated with a gene whose

CC expression is to be modulated and/or a ligand binding domain (LBD)

CC comprising a LBD from a nuclear receptor and a second gene expression

CC cassette capable of being expressed in a host cell comprising a

CC polynucleotide sequence encoding a second polypeptide comprising a trans-

CC activation domain and/or a LBD comprising a LBD from a nuclear receptor

CC other than ultraspriacle (USP) (the trans-activation domain is from a

CC nuclear receptor other than an ecdysone receptor, a retinoid X receptor

CC or a USP receptor and the LBDs from the first and second polypeptides are

CC different and dimerize). The ecdysone and retinoid X receptor based

CC inducible gene expression systems useful for modulating gene expression

CC in host cells, for use in gene therapy, large scale production of

CC proteins and antibodies, cell-based high-throughput screening assays

CC (HTS), functional genomic and regulation of traits in transgenic plants

CC and animals. The present sequence represents promoter from human

CC respiratory syncytial virus (RSV) which is used in an inducible gene

CC expression system of the invention

XX

XX Sequence 262 BP; 79 A; 53 C; 64 G; 66 T; 0 U; 0 Other;

Query Match 49.2%; Score 257.2; DB 4; Length 262;

Best Local Similarity 98.9%; Pred. No. 6.2e-80;

Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTCAACATGTAACGATGAGTTAGCAACAT 320

Db 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTCAACATGTAACGATGAGTTAGCAACAT 60

QY 321 GCCTTACAAGGAGAGAAAAAGCAACCGTCATGCCGATTTGGTGAAGTAAGGTGTGATCAT 380

Db 61 GCCTTACAAGGAGAGAAAAAGCAACCGTCATGCCGATTTGGTGAAGTAAGGTGTGATCAT 120

QY 381 CGTGCCTTATTAGGAGAGCAACAGACGGGCTCTGACATGGATTGGACGACCACTAAATTC 440

Db 121 CGTGCCTTATTAGGAGAGCAACAGACGGGCTCTGACATGGATTGGACGACCACTAAATTC 180

QY 441 CGCATTCGACAGATATTGTAATTTAAAGTGCTAGCTCGATACATAAAGCCATTTGACCA 500

Db 181 CGCATTCGACAGATATTGTAATTTAAAGTGCTAGCTCGATACATAAAGCCATTTGACCA 240

QY 501 TTCACACATTTGGTGTGCACT 522

Db 241 TTCACACATTTGGTGTGCACT 262

RESULT 61

AAQ06310

ID AAQ06310 standard; DNA; 3188 BP.

XX AAQ06310;

AC

XX 25-MAR-2003 (revised)

DT 29-JAN-1991 (first entry)

XX

XX Sequence of plasmid p79DBAM.

DE

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

KW hypersensitivity; ds.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH 279..335

FT LTR

FT polyA\_signal

FT 497..502

FT /\*tag= a

XX /\*tag= b

PN EP393502-A.

XX

XX 24-OCT-1990.

PD

XX 11-APR-1990; 90EP-00106992.

XX

XX 19-APR-1989; 89EP-00810295.

PR

XX (HOFF ) HOFFMANN-LA ROCHE AG.

PA

XX Fountoulak M, Garotta G, Stuber D;

PI WPI; 1990-322042/43.

XX

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,

PT chronic inflammations, etc.

PT

XX Disclosure; Fig 49; 174pp; English.

PS

XX IFN-gamma is a therapeutically active agent in the treatment of

CC autoimmune disease, allograft transplant rejections, multiple sclerosis,

CC chronic inflammations and delayed hypersensitivity. It is also useful in

CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.

CC (Updated on 25-MAR-2003 to correct PR field.)

XX

XX Sequence 3188 BP; 797 A; 774 C; 882 G; 735 T; 0 U; 0 Other;

Query Match

Best Local Similarity

Matches 288; Conservative

0; Mismatches 15; Indels 2;



QY 220 CTCAGGATATAGTATTCGCTTTTCATAGAGGGGAAATGATGCTTATGCAATAC 279  
 Db 5 CTCAGGATATAGTATTCGCTTTTCATAGAGGGGAAATGATGCTTATGCAATAC 64  
 QY 280 TCTTGTAGTCTTGCACATG-----GTAACGATGATGTTAGCAACATGCTTACAGGAGA 334  
 Db 65 TCTTGTAGTCTTGCACATGCTTATGTAACGATGATGTTAGCAACATGCTTACAGGAGA 124  
 QY 335 GAAAACACCGCTGATCCGATTCGTTGGAGTGAAGTGTAGCATGCTGCTTATTAGG 394  
 Db 125 GAAAACACCGCTGATCCGATTCGTTGGAGTGAAGTGTAGCATGCTGCTTATTAGG 183  
 QY 395 AAGCAACACGAGCGGTCTGACATGATGAGCAACCACTAAATTCGCGATTGCAGAGAT 454  
 Db 184 AAGCAACACGAGCGGTCTGACATGATGAGCAACCACTAAATTCGCGATTGCAGAGAT 243  
 QY 455 ATTGTATTTAAGTGGCTAGCTCGATACAAATAAAGCCATTTGACCAATTCACCAATTGGT 514  
 Db 244 ATTGTATTTAAGTGGCTAGCTCGATACAAATAAAGCCATTTGACCAATTCACCAATTGGT 303  
 QY 515 GTGCACCTC 523  
 Db 304 GTGCACCTC 312

RESULT 62  
 AAQ06311  
 ID AAQ06311 standard; DNA; 3276 BP.  
 XX  
 AC AAQ06311;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX  
 DE Sequence of plasmid p238BGL.

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 KW hypersensitivity; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS 243..426  
 FT /\*tag= b  
 FT Sig-peptide 243..405  
 FT /\*tag= c  
 FT /\*label= S.P.1  
 FT LTR 279..242  
 FT /\*tag= a  
 FT polyA\_signal 585..590  
 FT /\*tag= d  
 XX  
 PN EP393502-A.  
 XX  
 XX 24-OCT-1990.  
 XX  
 XX 11-APR-1990; 90EP-00106992.  
 XX  
 XX 19-APR-1989; 89EP-00810295.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX  
 XX Fountoulak M, Garotta G, Stuber D;  
 XX  
 XX WPI; 1990-322042/43.  
 DR P-PSDB; AAR07066.  
 XX  
 XX Soluble interferon-gamma receptors - for treating auto-immune diseases,  
 PT chronic inflammations, etc.  
 XX  
 XX Disclosure; fig 51; 174pp; English.  
 PS  
 XX

CC IFN-gamma is a therapeutically active agent in the treatment of  
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,  
 CC chronic inflammations and delayed hypersensitivity. It is also useful in  
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 3276 BP; 814 A; 794 C; 914 G; 754 T; 0 U; 0 Other;  
 Query Match 48.4%; Score 253; DB 2; Length 3276;  
 Best Local Similarity 93.2%; Pred. No. 7e-78; Indels 6; Gaps 2;  
 Matches 288; Conservative 0; Mismatches 15;  
 QY 220 CTCAGGATATAGTATTCGCTTTTCATAGAGGGGAAATGATGCTTATGCAATAC 279  
 Db 5 CTCAGGATATAGTATTCGCTTTTCATAGAGGGGAAATGATGCTTATGCAATAC 64  
 QY 280 TCTTGTAGTCTTGCACATG-----GTAACGATGATGTTAGCAACATGCTTACAGGAGA 334  
 Db 65 TCTTGTAGTCTTGCACATGCTTATGTAACGATGATGTTAGCAACATGCTTACAGGAGA 124  
 QY 335 GAAAACACCGCTGATCCGATTCGTTGGAGTGAAGTGTAGCATGCTGCTTATTAGG 394  
 Db 125 GAAAACACCGCTGATCCGATTCGTTGGAGTGAAGTGTAGCATGCTGCTTATTAGG 183  
 QY 395 AAGCAACACGAGCGGTCTGACATGATGAGCAACCACTAAATTCGCGATTGCAGAGAT 454  
 Db 184 AAGCAACACGAGCGGTCTGACATGATGAGCAACCACTAAATTCGCGATTGCAGAGAT 243  
 QY 455 ATTGTATTTAAGTGGCTAGCTCGATACAAATAAAGCCATTTGACCAATTCACCAATTGGT 514  
 Db 244 ATTGTATTTAAGTGGCTAGCTCGATACAAATAAAGCCATTTGACCAATTCACCAATTGGT 303  
 QY 515 GTGCACCTC 523  
 Db 304 GTGCACCTC 312

RESULT 63  
 AAQ06309  
 ID AAQ06309 standard; DNA; 3383 BP.  
 XX  
 AC AAQ06309;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX  
 DE Sequence of plasmid p76BGL.  
 XX  
 KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 KW hypersensitivity; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT LTR 279..504  
 FT /\*tag= a  
 FT CDS 505..540  
 FT /\*tag= b  
 FT polyA\_signal 692..697  
 FT /\*tag= c  
 XX  
 PN EP393502-A.  
 XX  
 XX 24-OCT-1990.  
 XX  
 XX 11-APR-1990; 90EP-00106992.  
 XX  
 XX 19-APR-1989; 89EP-00810295.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX  
 XX Fountoulak M, Garotta G, Stuber D;  
 XX

DR WPI; 1990-322042/43.  
 DR P-PSDB; AAR07065.  
 XX Soluble interferon-gamma receptors - for treating auto-immune diseases,  
 PT chronic inflammations, etc.  
 XX Disclosure; Fig 47; 174pp; English.  
 XX IFN-gamma is a therapeutically active agent in the treatment of  
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,  
 CC chronic inflammations and delayed hypersensitivity. It is also useful in  
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 XX Sequence 3383 BP; 838 A; 828 C; 929 G; 788 T; 0 U; 0 Other;  
 SQ  
 Query Match 48.4%; Score 253; DB 2; Length 3383;  
 Best Local Similarity 93.2%; Pred. No. 7.1e-78;  
 Matches 288; Conservative 0; Mismatches 15; Indels 6; Gaps 2;  
 XX  
 QY 220 CTCAGGATATAGTCTTCGCTTTTCGATAGGAGGGGAAATGTAGTCTTATGCAATAC 279  
 Db 5 CTCAGGATATAGTCTTCGCTTTTCGATAGGAGGGGAAATGTAGTCTTATGCAATAC 64  
 QY 280 TCTTGTAGTCTTCGCAACATG-----GTAACGATGAGTTAGCAACATGCTTTACAAGGAGA 334  
 Db 65 TCTTGTAGTCTTCGCAACATGCTTATGTAACGATGAGTTAGCAACATGCTTTACAAGGAGA 124  
 QY 335 GAAAGACACCGTGTGCGATGTTGGAAGTAAGTGTGATGCTGCTTATTAGG 394  
 Db 125 GAAAGACACCGTGTGCGATGTTGGAAGTAAGTGTGATGCTGCTTATTAGG 183  
 QY 395 AAGGCAACAGACCGTGTGCGATGTTGGAAGTAAGTGTGATGCTGCTTATTAGG 454  
 Db 184 AAGGCAACAGACCGTGTGCGATGTTGGAAGTAAGTGTGATGCTGCTTATTAGG 243  
 QY 455 ATTGTATTTAAGTGTGCTAGTCTGATACATATAAAGCCATTGACCATTCACCAATGGT 514  
 Db 244 ATTGTATTTAAGTGTGCTAGTCTGATACATATAAAGCCATTGACCATTCACCAATGGT 303  
 QY 515 GTGCACCTC 523  
 Db 304 GTGCACCTC 312  
 RESULT 64  
 AAQ06313  
 ID AAQ06313 standard; DNA; 3427 BP.  
 XX  
 AC AAQ06313;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX  
 XX Sequence of plasmid p267BGL.  
 XX  
 XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 KW hypersensitivity; ds.  
 XX  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX LTR 279..492  
 XX /\*tag= a  
 XX CDS 493..585  
 XX /\*tag= b  
 XX Sig-peptide 493..564  
 XX /\*tag= c  
 XX /label= S.P.2  
 XX polyA\_signal 736..741  
 XX /\*tag= d  
 XX  
 XX EF393502-A.

XX 24-OCT-1990.  
 XX  
 XX 11-APR-1990; 90EP-00106992.  
 XX  
 XX 19-APR-1989; 89EP-00810295.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX  
 XX Pountoulak M, Garotta G, Stuber D;  
 XX WPI; 1990-322042/43.  
 DR P-PSDB; AAR07067.  
 XX  
 XX Soluble interferon-gamma receptors - for treating auto-immune diseases,  
 PT chronic inflammations, etc.  
 XX Disclosure; Fig 59; 174pp; English.  
 XX  
 CC IFN-gamma is a therapeutically active agent in the treatment of  
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,  
 CC chronic inflammations and delayed hypersensitivity. It is also useful in  
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 XX Sequence 3427 BP; 846 A; 840 C; 942 G; 799 T; 0 U; 0 Other;  
 SQ  
 Query Match 48.4%; Score 253; DB 2; Length 3427;  
 Best Local Similarity 93.2%; Pred. No. 7.1e-78;  
 Matches 288; Conservative 0; Mismatches 15; Indels 6; Gaps 2;  
 XX  
 QY 220 CTCAGGATATAGTCTTCGCTTTTCGATAGGAGGGGAAATGTAGTCTTATGCAATAC 279  
 Db 5 CTCAGGATATAGTCTTCGCTTTTCGATAGGAGGGGAAATGTAGTCTTATGCAATAC 64  
 QY 280 TCTTGTAGTCTTCGCAACATG-----GTAACGATGAGTTAGCAACATGCTTTACAAGGAGA 334  
 Db 65 TCTTGTAGTCTTCGCAACATGCTTATGTAACGATGAGTTAGCAACATGCTTTACAAGGAGA 124  
 QY 335 GAAAGACACCGTGTGCGATGTTGGAAGTAAGTGTGATGCTGCTTATTAGG 394  
 Db 125 GAAAGACACCGTGTGCGATGTTGGAAGTAAGTGTGATGCTGCTTATTAGG 183  
 QY 395 AAGGCAACAGACCGTGTGCGATGTTGGAAGTAAGTGTGATGCTGCTTATTAGG 454  
 Db 184 AAGGCAACAGACCGTGTGCGATGTTGGAAGTAAGTGTGATGCTGCTTATTAGG 243  
 QY 455 ATTGTATTTAAGTGTGCTAGTCTGATACATATAAAGCCATTGACCATTCACCAATGGT 514  
 Db 244 ATTGTATTTAAGTGTGCTAGTCTGATACATATAAAGCCATTGACCATTCACCAATGGT 303  
 QY 515 GTGCACCTC 523  
 Db 304 GTGCACCTC 312  
 RESULT 65  
 AAQ06312  
 ID AAQ06312 standard; DNA; 3979 BP.  
 XX  
 AC AAQ06312;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX  
 XX Sequence of plasmid p264BGL.  
 XX  
 XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 KW hypersensitivity; ds.  
 XX  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX LTR 279..492  
 XX /\*tag= a  
 XX CDS 493..585  
 XX /\*tag= b  
 XX Sig-peptide 493..564  
 XX /\*tag= c  
 XX /label= S.P.2  
 XX polyA\_signal 736..741  
 XX /\*tag= d  
 XX  
 XX EF393502-A.

```
FT CDS 243..426
PT /*tag= b
PT Sig-peptide 243..405
PT /*tag= c
FT LTR 279..242
FT /*label= S.P.1
FT /*tag= a
FT polyA_signal 1288..1292
FT /*tag= d
XX EP393502-A.
XX
XX 24-OCT-1990.
XX
XX 11-APR-1990; 90EP-00106992.
XX
XX 19-APR-1989; 89EP-00810295.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Fountoulak M, Garotta G, Stuber D;
XX
XX WPI; 1990-322042/43.
XX
XX P-PSDB; AAR07066.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
XX chronic inflammations, etc.
XX
XX Disclosure; Fig 55; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment of
XX autoimmune disease, allograft transplant rejections, multiple sclerosis,
XX chronic inflammations and delayed hypersensitivity. It is also useful in
XX identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 3979 BP; 947 A; 987 C; 1113 G; 932 T; 0 U; 0 Other;
XX
XX Query Match 48.4%; Score 253; DB 2; Length 3979;
XX Best Local Similarity 93.2%; Pred. No. 7.7e-78;
XX Matches 288; Conservative 0; Mismatches 15; Indels 5; Gaps 2;
XX
XX QY 220 CTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATAC 279
XX |
XX Db 5 CTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATAC 64
XX |
XX QY 280 TCTTGTAGTCTTGCACATG----GTAAGATGATTAGCAACATGCCCTTACAGGAGA 334
XX |
XX Db 65 TCTTGTAGTCTTGCACATGCTTATGTACGATGATTAGCAACATGCCCTTACAGGAGA 124
XX |
XX QY 335 GAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGATCGTGCTTTATAGG 394
XX |
XX Db 125 GAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGATCGTGCTTTATAGG 183
XX |
XX QY 395 AAGGACACACACGGGCTGACATGGATTGGACGACACCACTAAATTCGCGATTCGAGAGAT 454
XX |
XX Db 184 AAGGACACACACGGGCTGACATGGATTGGACGACACCACTAAATTCGCGATTCGAGAGAT 243
XX |
XX QY 455 ATTGTATTATTAAAGTGGCTAGCTCGATACAAATAAAGCCCAATTTGACCAATTCACCAATTTGGT 514
XX |
XX Db 244 ATTGTATTATTAAAGTGGCTAGCTCGATACAAATAAAGCCCAATTTGACCAATTCACCAATTTGGT 303
XX |
XX QY 515 GTGCACCTC 523
XX |
XX Db 304 GTGCACCTC 312
XX |
XX
XX RESULT 66
XX ACD27899
XX ID ACD27899 standard; DNA; 10468 BP.
XX AC
XX ACD27899;
XX
```

```
DT 25-SEP-2003 (first entry)
XX
XX pdmT2 vector DNA sequence useful as a lentiviral vector.
XX
XX Lentiviral vector; transcriptional regulatory sequence; endothelial cell;
XX VSV glycoprotein envelope; gene delivery; angiogenesis related pathology;
XX vesicular stomatitis virus; selective gene expression; tissue ischaemia;
XX gene therapy; retinal neovascularisation; chronic inflammatory disorder;
XX tumor; metastasis; cytostatic; antiinflammatory; vasotropic; pdmT2;
XX lentivirus; human cytomegalovirus; HCMV; mouse; human; mutant; ds.
XX
XX Lentivirus sp.
XX Mus sp.
XX Homo sapiens.
XX Human cytomegalovirus.
XX Synthetic.
XX
XX US2003095948-A1.
XX
XX 22-MAY-2003.
XX
XX 28-MAY-2002; 2002US-00155736.
XX
XX 29-MAY-2001; 2001IT-MI001138.
XX
XX (UYTO-) UNIV TORINO.
XX
XX Naldini L, Palma MD;
XX
XX WPI; 2003-558321/52.
XX
XX New lentiviral vector construct for transferring nucleotide sequences in
XX vivo and ex vivo, useful for treating tissue ischemia, retinal
XX neovascularization, chronic inflammatory disorders, tumor or metastasis.
XX
XX Example; Fig 9A-9D; 21pp; English.
XX
XX The present invention relates to a lentiviral vector construct for
XX transferring nucleotide sequences in vivo and ex vivo. The vector
XX comprises transcriptional regulatory sequences of one or more genes
XX preferentially expressed in the endothelial cells of mammals. The
XX lentiviral vector also comprises a vesicular stomatitis virus (VSV)
XX glycoprotein envelope that transduces the transfer of the vector
XX construct. The lentiviral vector is useful for treating an angiogenesis
XX related pathology by gene delivery and selective expression of a gene in
XX cells engaged in angiogenesis. The lentiviral vector construct is useful
XX for treating tissue ischaemia, retinal neovascularisation, chronic
XX inflammatory disorders, tumors or metastasis. The present sequence
XX represents pdmT2 vector which may be used as a lentiviral vector
XX
XX Sequence 10468 BP; 2764 A; 2437 C; 2638 G; 2629 T; 0 U; 0 Other;
XX
XX Query Match 41.6%; Score 217.4; DB 8; Length 10468;
XX Best Local Similarity 99.1%; Pred. No. 4.6e-65;
XX Matches 229; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
XX QY 260 AATGATGCTTATGCAATACCTTTGTAGCTTGCACATGTAACGATGATTAGCAACA 319
XX |
XX Db 2217 AATGATGCTTATGCAATACCTTTGTAGCTTGCACATGTAACGATGATTAGCAACA 2276
XX |
XX QY 320 TGCCTTACAGGAGAGAAAAGCCCGTCGATGCCGATTTGGTGAAGTAAAGTGGTACGA 379
XX |
XX Db 2277 TGCCTTACAGGAGAGAAAAGCCCGTCGATGCCGATTTGGTGAAGTAAAGTGGTACGA 2336
XX |
XX QY 380 TCGTGCCCTTATTAGGAAGCAACAGACGGGTCTGCATGCGATTGCGAACCACTAAATT 439
XX |
XX Db 2337 TCGTGCCCTTATTAGGAAGCAACAGACGGGTCTGCATGCGATTGCGAACCACTGATT 2396
XX |
XX QY 440 -CCGATTGCGAGATATTGTTATTAAAGTCCCTAGCTCGATACATAAATACG 489
XX |
XX Db 2397 GCCCGATTGCGAGATATTGTTATTAAAGTCCCTAGCTCGATACATAAATACG 2447
XX |
```

RESULT 67  
AAC92489  
ID AAC92489 standard; DNA; 858 BP.  
XX  
AC AAC92489;  
XX  
DT 26-MAR-2001 (first entry)  
XX  
DE Fragment of RSV DNA including tandem repeat LTR and non-coding region.  
XX  
KW Integrase; transgenic animal; transgenic bird; gene therapy; cancer; ds.  
XX  
OS Rous sarcoma virus.  
XX  
PN WO200075342-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 27-APR-2000; 2000WO-JP002785.  
XX  
PR 04-JUN-1999; 99JP-00158351.  
XX  
PA (NIPP) NIPPON INST BIOLOGICAL SCIENCE.  
XX  
PI Katsumata A, Hoshi S, Ihara T, Ueda S;  
XX  
DR WPI; 2001-061729/07.  
XX  
XX Plasmid vector for efficient insertion of foreign DNA into host cells to  
PT give transforms with stable quality, useful e.g. in producing DNA  
PT vaccines on large scale, and in gene therapy with ease and safely and  
PT without pathogenicity.  
XX  
PS Disclosure; Page 88-99; 94pp; Japanese.  
XX  
CC This invention relates to a vector which consists of an integrase gene, a  
CC regulatory region of DNA involved in the expression of the integrase  
CC gene, and a DNA fragment constituting a recognition region used in the  
CC catalysis of the integrase in the integrase reaction. The invention  
CC includes methods for the production of transgenic animals and birds using  
CC the vector of the invention. The plasmid vector can be for inserting  
CC foreign DNA into host cells to yield transformants. The transformants may  
CC be useful in producing DNA vaccines, and in gene therapy against cancer,  
CC congenital genetic diseases or infections. The present sequence  
CC represents a fragment of DNA from Rous sarcoma virus, including tandem  
CC repeat LTRs and adjacent non-coding region. The DNA fragment is used in  
CC the production of the vector of the invention.  
XX  
SQ Sequence 858 BP; 215 A; 202 C; 246 G; 195 T; 0 U; 0 Other;  
Query Match 40.6%; Score 212.2; DB 5; Length 858;  
Best Local Similarity 88.1%; Pred. No. 8.5e-64;  
Matches 260; Conservative 0; Mismatches 18; Indels 17; Gaps 2;  
QY 245 GCATAGGAGGGGGAATAGTCTTATGCAATACTCTTGTAGTCTTCCACATG----- 299  
DB 200 GCAGAGGCTTCAATTAATAGTCTTATGCAATACTCTTGTAGTCTTCCACATGCTTAT 259  
QY 300 GTAAAGTATGTTAGTACGCTTCAAGAGAGAGAAAGCAGCCGTCGCGATG 359  
DB 260 GTAAAGTATGTTAGTACGCTTCAAGAGAGAGAAAGCAGCCGTCGCGATG 319  
QY 360 GTGGAATAGGT-----GGTACGATCGCTCTTATAGGAGGCAACAGAG 407  
DB 320 GTGGAATAGGTGATGATCTAGTACGATCGTCTTATAGGAGGCAACAGAG 379  
QY 408 GGTCTGACATGATGGAAGCAACCTAAATCCGATTCGAGAGATTTGATTTAAGT 467  
DB 380 GGTCTAAGCAGATTTGGAAGCAACCTAAATCCGATTCGAGAGATTTGATTTAAGT 439  
QY 468 GCCTAGCTCGATACATAAGCGCATTTGACCATTCACCATTTGGTGTGACCT 522  
DB 440 GCCTAGCTCGATACATAAGCGCATTTTACCATTCACCATTTGGTGTGACCT 494

RESULT 68  
AAX77359  
ID AAX77359 standard; DNA; 9542 BP.  
XX  
AC AAX77359;  
XX  
DT 09-AUG-1999 (first entry)  
XX  
DE Polynucleotide sequence of 987 BB neo.  
XX  
KW Nucleic acid identification; exogenous protein; gene sorting;  
XX growth factor; membrane receptor; sindbis virus; ss.  
XX  
OS Synthetic.  
XX  
PN WO925876-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 17-NOV-1998; 98WO-US024520.  
XX  
PR 17-NOV-1997; 97US-00972218.  
XX  
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.  
XX  
PI Bailey JE, Renner WA, Orberger GH, Koller D;  
XX  
DR WPI; 1999-357620/30.  
XX  
PT Isolating genes encoding proteins with selected properties, useful for  
PT identifying therapeutic agents or targets.  
XX  
PS Disclosure; Fig 13A-C; 136pp; English.  
XX  
CC The invention relates to the identification of a recombinant nucleic acid  
CC encoding an exogenous protein having a selected property. The method  
CC comprises preparing a population of eukaryotic host cells, culturing the  
CC cells under suitable conditions and identifying cells that contain the  
CC recombinant nucleic acid. The method is used to sort genes according to  
CC the type of proteins they express, and also to identify new ligand/  
CC receptor interactions. Typical applications of the nucleic acid and the  
CC exogenous protein are in isolation of new growth factors, cytokines,  
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of  
CC which may be useful as therapeutic agents or therapeutic targets, e.g.  
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell  
CC proliferation or metabolic processes etc. The protein can also be used as  
CC screen for specific modulators. The nucleic acid can also be used as  
CC sources of therapeutic antisense or ribozyme sequences. The method allows  
CC the protein (rather than a partial DNA sequence) to be isolated and,  
CC since a wide range of cells can be used, they can be expressed with the  
CC correct glycosylation pattern  
XX  
SQ Sequence 9542 BP; 2463 A; 2516 C; 2387 G; 2176 T; 0 U; 0 Other;  
Query Match 39.2%; Score 205.2; DB 2; Length 9542;  
Best Local Similarity 98.6%; Pred. No. 8.8e-61;  
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 261 ATGTAGTCTTATGCAATACTCTTGTAGTCTTGTGCAATGTTACGATGATGACACAT 320  
DB 665 ATCCAGTCTTATGCAATACTCTTGTAGTCTTGTGCAATGTTACGATGATGACACAT 724  
QY 321 GCCTTACAGGAGAGAAAGCCCGTCGATGCCGATGCTGAGTAGTGGTAGCAT 380  
DB 725 GCCTTACAGGAGAGAAAGCCCGTCGATGCCGATGCTGAGTAGTGGTAGCAT 784  
QY 381 CGTCCCTTATAGGAGGCAACGAGCGGTCTGATGATGTTGGACGACCACTAAATTC 440  
DB 795 CGTCCCTTATAGGAGGCAACGAGCGGTCTGATGATGTTGGACGACCACTAAATTC 844  
QY 441 CGCATTCGAGAGATATTGTTAATTAAGTGCC 470

Db	845	CGCATTGCAGAGATTTGTTATTAGTGCC	874
Db	321	GCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGGAAAGTAAGGTGCTACGAT	380
Db	725	GCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGGAAAGTAAGGTGCTACGAT	784
Qy	381	CGTGCCTTTATTAGGAAGGCAACAGACGGGTCGTGACATGGATTGGACGAACCACTAAATTC	440
Db	785	CGTGCCTTTATTAGGAAGGCAACAGACGGGTCGTGACATGGATTGGACGAACCACTAAATTC	844
Qy	441	CGCATTGCAGAGATTTGTTATTAGTGCC	470
Db	845	CGCATTGCAGAGATTTGTTATTAGTGCC	874
RESULT 70			
AAZ27850			
ID	AAZ27850	standard; cDNA; 11282 BP.	
XX	AAZ27850;		
AC	AAZ27850;		
XX	23-DEC-1999	(first entry)	
XX	Complete cDNA sequence of pCYTts.		
XX	Gene expression system; cis-acting element; gene therapy;		
KW	temperature-sensitive RNA-dependent RNA polymerase;		
KW	inducible alphaviral gene expression system; pCYTts;		
KW	hormone-based gene control system; tetracycline gene control system; ss.		
XX	Synthetic.		
OS			
XX	WO950432-A1.		
PN	07-OCT-1999.		
XX	25-MAR-1999;	99WO-IB000523.	
XX	27-MAR-1998;	98US-0079562P.	
XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.		
PA	(RENN/) RENNER W A.		
PA	(NIEB/) NIEBA L.		
PA	(BOOR/) BOORSMA M.		
PI	Renner WA, Nieba L, Boorsma M;		
XX	MPI; 1999-591327/50.		
XX	A new system to regulate gene expression in eukaryotic cells.		
PS	Claim 15; Fig 3; 99pp; English.		
XX	This sequence represents the complete cDNA sequence for the vector		
CC	pCYTts. The invention relates to a DNA molecule comprising a		
CC	polynucleotide (I) encoding an RNA molecule. The encoded RNA comprises:		
CC	(a) at least one cis-acting element; (b) an open reading frame (ORF1)		
CC	encoding a non-cytopathic, temperature-sensitive RNA-dependent RNA		
CC	polymerase; and (c) a second sequence that is: (i) a protein-encoding ORF		
CC	(ORF2) that is in a translatable format after RNA-dependent RNA		
CC	replication event(s); (ii) a sequence complementary to the ORF2; or (iii)		
CC	a sequence encoding an untranslated RNA molecule. The pCYTts sequence is		
CC	an example of the DNA molecule, and is an inducible alphaviral gene		
CC	expression system. The invention is used in gene therapy and recombinant		
CC	technology to regulate expression of introduced genes. The invention does		
CC	not have the problems of toxicity and/or high basal level expression		
CC	associated with prior art tetracycline-based and hormone-based gene		
CC	control systems		
XX	Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;		
Query Match	39.2%;	Score 205.2; DB 2; Length 11282;	
Best Local Similarity	98.6%;	Pred. No. 9.6e-61;	
Matches	207; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	

QY 261 ATGTAGTCTTATGCAATACCTCTGTAGTCTTGCACATGCTAACGATGAGTTAGCAACAT 320  
Db |||||  
664 ATCCAGTCTTATGCAATACCTCTGTAGTCTTGCACATGCTAACGATGAGTTAGCAACAT 723  
QY 321 GCCTTACAGGAGAGAAAAGCAACCGTGATGCCGATGCTGTGAAGTAAAGTGTGACGAT 380  
Db |||||  
724 GCCTTACAGGAGAGAAAAGCAACCGTGATGCCGATGCTGTGAAGTAAAGTGTGACGAT 783  
QY 381 CGTGCTTATTAGGAAGGCAACAGACCGGTCTGACATGATGGAGCAACCACTAAATTC 440  
Db |||||  
784 CGTGCTTATTAGGAAGGCAACAGACCGGTCTGACATGATGGAGCAACCACTAAATTC 843  
QY 441 CGCATTCGAGAGATATGTTTAAAGTGCC 470  
Db 844 CGCATTCGAGAGATATGTTTAAAGTGCC 873

## RESULT 71

AAD04741  
ID AAD04741 standard; cDNA; 11282 BP.

XX  
AC AAD04741;  
XX  
DT 17-JUL-2001 (first entry)  
XX  
DE Alphaviral vector pCYTts cDNA.  
XX  
KW pCYTts; alphaviral vector; vaccine; therapy; cancer; antiparasitic;  
KW antimalarial; anticancer; anti-HIV; antiviral; infectious disease;  
KW human immunodeficiency virus; HIV; influenza; passive immunisation;  
KW carcinoma; liver; skin; stomach; ovarian tumour; ss.

OS Rous sarcoma virus.

OS Alphavirus.

OS Unidentified.

OS Chimeric.

XX WO200130989-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-IB001557.

XX 27-OCT-1999; 99US-0161796P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (RENN/) RENNER W A.

PA (NIEB/) NIEBA L.

XX Renner WA, Nieba L;

XX WPI; 2001-308631/32.

XX Preparing alphaviral vectors with mutations in a selected gene, for use  
PT as vaccines, particularly against pathogens that mutate rapidly,  
PT comprises replicating in the presence of a nucleoside analog.  
XX  
PS Claim 6; Fig 3; 103pp; English.

XX The present invention relates to a method for preparing viral vectors  
CC which comprises inserting a gene of interest into an alphaviral vector  
CC such as pCYTts, pSINKps and replicating the vector in the presence of  
CC alphaviral replicase and nucleoside analogues (5'-azacytidine (AZT), FU-  
CC 5', fluorouridine) to produce a modified gene of interest. The replication  
CC is repeated until the modified gene in 90 % of the vector population  
CC contain a mutation in the modified gene which is 90-99 % identical with  
CC the gene of interest. The vector populations are used in vaccines for  
CC treatment or prevention of a wide variety of infectious diseases (viral  
CC or parasitic, e.g. human immunodeficiency virus (HIV), influenza,  
CC Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach  
CC carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the  
CC mutant populations will therefore be effective against viral escape  
CC mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins

CC are correctly glycosylated. Antisera raised against the vaccines can be  
CC used for passive immunisation. The present cDNA sequence is an alphaviral  
CC vector pCYTts. The vector contains Rous Sarcoma Virus promoter, cis-  
CC acting sequence elements, non-structural proteins 1-4, gene of interest,  
CC alphavirus subgenomic promoter, ampicillin resistance marker for  
CC selection and a CoIE1 sequence for bacterial amplification  
XX

SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 39.2%; Score 205.2; DB 4; Length 11282;  
Best Local Similarity 98.6%; Pred. No. 9.6e-61;  
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATACCTCTGTAGTCTTGCACATGCTAACGATGAGTTAGCAACAT 320

Db |||||

664 ATCCAGTCTTATGCAATACCTCTGTAGTCTTGCACATGCTAACGATGAGTTAGCAACAT 723

QY 321 GCCTTACAGGAGAGAAAAGCAACCGTGATGCCGATGCTGTGAAGTAAAGTGTGACGAT 380

Db |||||

724 GCCTTACAGGAGAGAAAAGCAACCGTGATGCCGATGCTGTGAAGTAAAGTGTGACGAT 783

QY 381 CGTGCTTATTAGGAAGGCAACAGACCGGTCTGACATGATGGAGCAACCACTAAATTC 440

Db |||||

784 CGTGCTTATTAGGAAGGCAACAGACCGGTCTGACATGATGGAGCAACCACTAAATTC 843

QY 441 CGCATTCGAGAGATATGTTTAAAGTGCC 470

Db 844 CGCATTCGAGAGATATGTTTAAAGTGCC 873

RESULT 72

AAF84024

ID AAF84024 standard; cDNA; 11282 BP.

XX  
AC AAF84024;

XX  
DT 22-AUG-2001 (first entry)

DE Complete cDNA sequence of plasmid pCYTt.

XX pCYTt; cellular; taxol; gene therapy; RNA replication; endogenous gene;

XX ss.

XX Synthetic.

XX WO200142442-A2.

XX 14-JUN-2001.

XX 08-DEC-2000; 2000WO-IB001841.

XX 10-DEC-1999; 99US-0169988P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Hennecke F, Renner WA;

XX WPI; 2001-381672/40.

XX Modifying endogenous target gene expression in eukaryotic cell for

PT performing gene therapy, involves inserting exogenous polynucleotides in

PT gene to produce recombinant eukaryotic host cell and culturing the cell.

XX Disclosure; Fig 8A-D; 131pp; English.

XX The invention relates to a method of modifying expression characteristics

CC of an endogenous target gene within a genome of a eukaryotic cell or

CC producing a polypeptide encoded by the target gene of a eukaryotic cell.

CC The method involves inserting exogenous polynucleotides in 5' and 3'

CC regions flanking the coding region of target gene to produce a

CC recombinant eukaryotic host cell, and culturing the cell. The method is

CC useful for producing cells which exhibit increased expression of

CC endogenous genes which lead to the production of additional products, and



PT U3 regions, a constitutive transport element, and a cloning site.  
XX Claim 18; Col 95-97; 61pp; English.  
XX The invention relates to novel retroviral vector plasmids for introducing  
CC expressible polynucleotides into cells. The vectors comprise a retrovirus  
CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive  
CC transport element (CTE) and a cloning site. The retroviral vector plasmid  
CC is useful in introducing an expressible polynucleotide into a cell such  
CC as a neural stem cell and in treating or ameliorating a pathologic  
CC condition in a subject such as a congenital diseases, cancer, Parkinson's  
CC disease or Alzheimer's disease. The plasmid may also be used to produce  
CC retroviral vectors useful for delivering genes into eukaryotic cells in  
CC culture and in living organisms. Sequences of the invention are also  
CC useful in gene therapy. The present sequence is MESV2/EGFP/RSV retroviral  
CC vector DNA  
XX  
SQ Sequence 4993 BP; 1206 A; 1328 C; 1303 G; 1156 T; 0 U; 0 Other;  
Query Match 33.5%; Score 175.2; DB 7; Length 4993;  
Best Local Similarity 98.3%; Pred. No. 2.4e-50;  
Matches 177; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 259 AAATGTAGTCTTATGCAATACACTTGTAGTCTTGTCAACATGTTAGCAAC 1966  
DB 1907 AAATGTAGTCTTATGCAATACACTTGTAGTCTTGTCAACATGTTAGCAAC 1966  
QY 319 ATGCGCTTACAGAGAGAGAAAAGCAGCGTGCATCCGATTTGGTGAAGTAAAGGTGTTACG 378  
DB 1967 ATGCGCTTACAGAGAGAGAAAAGCAGCGTGCATCCGATTTGGTGAAGTAAAGGTGTTACG 2026  
QY 379 ATCGTGCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTTGGACGACCACTAAAT 438  
DB 2027 ATCGTGCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTTGGACGACCACTAGAT 2086  
RESULT 75  
AAD53270  
ID AAD53270 standard; DNA; 5643 BP.  
XX  
AC AAD53270;  
XX  
DT 28-MAY-2003 (first entry)  
DE MESVR/ACTE/IRESEGFP retroviral vector DNA.  
XX  
XX Retroviral vector; congenital disease; cancer; Parkinson's disease;  
KW Alzheimer's disease; gene therapy; retroviral DNA; ds.  
XX  
OS Retrovirus.  
XX  
XX WO200294989-A2.  
XX  
XX 28-NOV-2002.  
XX  
XX 17-MAY-2002; 2002WO-US015816.  
XX  
XX 18-MAY-2001; 2001US-0292201P.  
XX  
XX 30-NOV-2001; 2001US-0334972P.  
XX  
XX (SCR ) SCRIPPS RES INST.  
XX  
XX Edelman GM, Owens G;  
XX  
XX WPI; 2003-140366/13.  
XX  
XX New retroviral vector plasmid for introducing expressible polynucleotides  
PT into cells, comprises a retrovirus long terminal repeat having U5, R and  
XX U3 regions, a constitutive transport element, and a cloning site.  
XX  
XX Claim 18; Col 88-91; 61pp; English.  
XX  
XX The invention relates to novel retroviral vector plasmids for introducing

CC expressible polynucleotides into cells. The vectors comprise a retrovirus  
CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive  
CC transport element (CTE) and a cloning site. The retroviral vector plasmid  
CC is useful in introducing an expressible polynucleotide into a cell such  
CC as a neural stem cell and in treating or ameliorating a pathologic  
CC condition in a subject such as a congenital diseases, cancer, Parkinson's  
CC disease or Alzheimer's disease. The plasmid may also be used to produce  
CC retroviral vectors useful for delivering genes into eukaryotic cells in  
CC culture and in living organisms. Sequences of the invention are also  
CC useful in gene therapy. The present sequence is MESVR/ACTE/IRESEGFP  
CC retroviral vector DNA  
XX  
SQ Sequence 5643 BP; 1356 A; 1505 C; 1472 G; 1310 T; 0 U; 0 Other;  
Query Match 33.5%; Score 175.2; DB 7; Length 5643;  
Best Local Similarity 98.3%; Pred. No. 2.5e-50;  
Matches 177; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 259 AAATGTAGTCTTATGCAATACACTTGTAGTCTTGTCAACATGTTAGCAAC 318  
DB 2557 AAATGTAGTCTTATGCAATACACTTGTAGTCTTGTCAACATGTTAGCAAC 2616  
QY 319 ATGCGCTTACAGAGAGAGAAAAGCAGCGTGCATCCGATTTGGTGAAGTAAAGGTGTTACG 378  
DB 2617 ATGCGCTTACAGAGAGAGAAAAGCAGCGTGCATCCGATTTGGTGAAGTAAAGGTGTTACG 2676  
QY 379 ATCGTGCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTTGGACGACCACTAAAT 438  
DB 2677 ATCGTGCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTTGGACGACCACTAGAT 2736

Search completed: March 11, 2004, 08:23:00  
Job time : 463.959 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

ON nucleic - nucleic search, using sw model

Run on: March 11, 2004, 08:11:32 ; Search time 96.6012 seconds  
(without alignments)  
3004.511 Million cell updates/sec

Title: US-09-733-368A-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgctccctgtgtgtgtt.....accacatggtgtgcacctc 523

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	98.5	4965	2	US-08-564-313-1
2	515	98.5	4965	5	PCT-US94-06069-1
3	505.6	96.7	4059	2	US-08-564-313-2
4	505.6	96.7	4059	5	PCT-US94-06069-2
5	505.6	96.7	5653	1	US-08-073-836-3
6	505.6	96.7	5653	1	US-08-235-277-1
7	505.6	96.7	8591	1	US-08-462-859A-6
8	505.6	96.7	8591	1	US-08-462-859A-8
9	505.6	96.7	8591	1	US-08-123-659A-6
10	505.6	96.7	8591	1	US-08-123-659A-8
11	505.6	96.7	8591	1	US-08-464-247A-6
12	505.6	96.7	8591	1	US-08-464-247A-8
13	505.6	96.7	8591	1	US-08-464-248A-6
14	505.6	96.7	8591	1	US-08-464-248A-8
15	500.8	95.8	6836	4	US-09-479-122-18
16	500.8	95.8	6836	4	US-09-484-997-18
17	500.8	95.8	6836	4	US-09-481-355-18
18	500.8	95.8	6836	4	US-09-481-355-18
19	500.8	95.8	6836	4	US-09-455-659A-18
20	500.8	95.8	6836	4	US-09-484-996-18
21	500.8	95.8	6836	4	US-09-479-123-18
22	500.8	95.8	6836	4	US-09-479-122-22
23	500.8	95.8	9737	4	US-09-479-122-23
24	500.8	95.8	9737	4	US-09-479-122-23
25	500.8	95.8	9737	4	US-09-484-997-22
26	500.8	95.8	9737	4	US-09-484-997-22
27	500.8	95.8	9737	4	US-09-484-997-28

Sequence 22, Appl	95.8	9737	4	US-09-481-355-22	Sequence 22, Appl	
Sequence 23, Appl	95.8	9737	4	US-09-481-355-23	Sequence 23, Appl	
Sequence 28, Appl	95.8	9737	4	US-09-481-355-28	Sequence 28, Appl	
Sequence 22, Appl	95.8	9737	4	US-09-481-282-22	Sequence 22, Appl	
Sequence 23, Appl	95.8	9737	4	US-09-481-282-23	Sequence 23, Appl	
Sequence 28, Appl	95.8	9737	4	US-09-481-282-28	Sequence 28, Appl	
Sequence 22, Appl	95.8	9737	4	US-09-455-659A-22	Sequence 22, Appl	
Sequence 23, Appl	95.8	9737	4	US-09-455-659A-23	Sequence 23, Appl	
Sequence 28, Appl	95.8	9737	4	US-09-455-659A-28	Sequence 28, Appl	
Sequence 22, Appl	95.8	9737	4	US-09-484-996-22	Sequence 22, Appl	
Sequence 23, Appl	95.8	9737	4	US-09-484-996-23	Sequence 23, Appl	
Sequence 28, Appl	95.8	9737	4	US-09-484-996-28	Sequence 28, Appl	
Sequence 22, Appl	95.8	9871	4	US-09-479-123-22	Sequence 22, Appl	
Sequence 23, Appl	95.8	9871	4	US-09-479-123-23	Sequence 23, Appl	
Sequence 28, Appl	95.8	9871	4	US-09-479-123-28	Sequence 28, Appl	
Sequence 24, Appl	95.8	9871	4	US-09-479-122-24	Sequence 24, Appl	
Sequence 24, Appl	95.8	9871	4	US-09-484-997-24	Sequence 24, Appl	
Sequence 24, Appl	95.8	9871	4	US-09-481-355-24	Sequence 24, Appl	
Sequence 24, Appl	95.8	9871	4	US-09-481-282-24	Sequence 24, Appl	
Sequence 24, Appl	95.8	9871	4	US-09-455-659A-24	Sequence 24, Appl	
Sequence 24, Appl	95.8	9871	4	US-09-479-123-24	Sequence 24, Appl	
Sequence 25, Appl	10060	95.8	10060	4	US-09-479-122-25	Sequence 25, Appl
Sequence 25, Appl	10060	95.8	10060	4	US-09-484-997-25	Sequence 25, Appl
Sequence 25, Appl	10060	95.8	10060	4	US-09-481-355-25	Sequence 25, Appl
Sequence 25, Appl	10060	95.8	10060	4	US-09-481-282-25	Sequence 25, Appl
Sequence 25, Appl	10060	95.8	10060	4	US-09-455-659A-25	Sequence 25, Appl
Sequence 25, Appl	10060	95.8	10060	4	US-09-484-996-25	Sequence 25, Appl
Sequence 25, Appl	10060	95.8	10060	4	US-09-479-123-25	Sequence 25, Appl
Sequence 13, Appl	90.2	565	4	US-09-167-322-13	Sequence 13, Appl	
Sequence 1, Appl	74.6	11627	4	US-09-470-881-1	Sequence 1, Appl	
Sequence 2, Appl	9521	3	3	US-08-972-218-2	Sequence 2, Appl	
Sequence 1, Appl	9521	4	4	US-09-193-707-2	Sequence 1, Appl	
Sequence 5, Appl	11282	3	3	US-09-733-042-1	Sequence 5, Appl	
Sequence 5, Appl	3853	3	3	US-08-801-092-5	Sequence 5, Appl	
Sequence 5, Appl	3853	3	3	US-09-315-113-5	Sequence 5, Appl	
Sequence 9, Appl	28.9	3925	3	US-09-011-745-9	Sequence 9, Appl	
Sequence 19, Appl	28.9	4026	3	US-08-801-092-19	Sequence 19, Appl	
Sequence 19, Appl	28.9	4026	3	US-09-315-113-19	Sequence 19, Appl	
Sequence 33, Appl	28.9	4249	3	US-08-801-092-33	Sequence 33, Appl	
Sequence 33, Appl	28.9	4249	3	US-09-315-113-33	Sequence 33, Appl	
Sequence 35, Appl	28.9	5053	4	US-09-311-784A-35	Sequence 35, Appl	
Sequence 1, Appl	28.9	5618	3	US-08-799-569-1	Sequence 1, Appl	
Sequence 1, Appl	28.9	5618	3	US-09-570-546-1	Sequence 1, Appl	
Sequence 1, Appl	28.9	5618	3	US-09-146-072A-1	Sequence 1, Appl	
Sequence 1, Appl	28.9	6200	4	US-09-439-923-1	Sequence 1, Appl	
Sequence 1, Appl	28.9	6200	4	US-09-711-202A-1	Sequence 1, Appl	
Sequence 5, Appl	28.9	6200	4	US-09-711-205A-1	Sequence 5, Appl	
Sequence 4, Appl	28.9	6338	4	US-08-627-151A-5	Sequence 4, Appl	
Sequence 6, Appl	28.9	6338	4	US-09-646-691B-4	Sequence 6, Appl	
Sequence 6, Appl	28.9	6896	2	US-08-809-513A-6	Sequence 6, Appl	
Sequence 8, Appl	28.9	7086	4	US-08-627-151A-6	Sequence 8, Appl	
Sequence 8, Appl	28.9	7086	4	US-09-935-194-1	Sequence 8, Appl	
Sequence 5, Appl	28.9	7106	1	US-08-188-281B-8	Sequence 5, Appl	
Sequence 5, Appl	28.9	7106	1	US-08-453-552-5	Sequence 5, Appl	
Sequence 5, Appl	28.9	7106	1	US-08-710-637-5	Sequence 5, Appl	
Sequence 8, Appl	28.9	7106	5	PCT-US93-00907-8	Sequence 8, Appl	
Sequence 8, Appl	28.9	7106	5	PCT-US94-07280-8	Sequence 8, Appl	
Sequence 8, Appl	28.9	7106	5	PCT-US95-01087-8	Sequence 8, Appl	
Sequence 3, Appl	28.9	7298	1	US-08-453-552-3	Sequence 3, Appl	
Sequence 3, Appl	28.9	7298	1	US-08-710-637-3	Sequence 3, Appl	
Sequence 3, Appl	28.9	7298	5	PCT-US93-00907-3	Sequence 3, Appl	
Sequence 4, Appl	28.9	7308	3	US-09-011-745-3	Sequence 4, Appl	
Sequence 4, Appl	28.9	7308	3	US-09-011-745-4	Sequence 4, Appl	
Sequence 12, Appl	28.9	8540	5	US-08-487-283A-4	Sequence 12, Appl	
Sequence 3, Appl	28.9	8540	5	PCT-US96-05611A-12	Sequence 3, Appl	
Sequence 5, Appl	28.9	8578	4	US-09-796-575-3	Sequence 5, Appl	
Sequence 5, Appl	28.9	8614	4	US-09-247-352-5	Sequence 5, Appl	
Sequence 6, Appl	28.9	8614	4	US-09-466-635-5	Sequence 6, Appl	
Sequence 6, Appl	28.9	8858	4	US-09-247-352-6	Sequence 6, Appl	
Sequence 6, Appl	28.9	8858	4	US-09-466-635-6	Sequence 6, Appl	
Sequence 8, Appl	28.9	8932	2	US-08-252-493C-8	Sequence 8, Appl	
Sequence 8, Appl	28.9	8932	3	US-09-276-197-8	Sequence 8, Appl	

## ALIGNMENTS

RESULT 1  
 US-08-564-313-1  
 ; Sequence 1, Application US/08564313  
 ; Patent No. 5910488  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nabel, Elizabeth  
 ; APPLICANT: Nabel, Gary  
 ; APPLICANT: Lew, Denise  
 ; APPLICANT: Marquet, Magda  
 ; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear  
 ; STREET: 620 Newport Center Drive 16th Floor  
 ; CITY: Newport Beach  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/564,313  
 ; FILING DATE: 01-DEC-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/074,344  
 ; FILING DATE: 07-JUN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Israel, Ned  
 ; REGISTRATION NUMBER: 29,655  
 ; REFERENCE/DOCKET NUMBER: VICAL.033CP1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4965 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: circular  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE:  
 ; IMMEDIATE SOURCE:  
 ; CLONE: HLA-B7 and Beta-2  
 ;

Query Match 98.5%; Score 515; DB 2; Length 4965;  
 Best Local Similarity 99.0%; Pred. No. 3.9e-174;  
 Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGTTGTGTGTGGAGTGTGCTAGTGTGCGGAGCAAAATTTAGCTTACA 60  
 Db 1 CTGCTCCCTGTTGTGTGTGGAGTGTGCTAGTGTGCGGAGCAAAATTTAGCTTACA 60  
 QY 61 ACAAGCGAGCTTGACCCACAATTCGATGCAAGAACTGCTTAGGGTTAGGGTTTGGC 120  
 Db 61 ACAAGCGAGCTTGACCCACAATTCGATGCAAGAACTGCTTAGGGTTAGGGTTTGGC 120  
 QY 121 CTGCTTCGCGATGTACGGGCCAGAGATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 121 CTGCTTCGCGATGTACGGGCCAGAGATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 180

QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTGGC 240  
 Db 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTGGC 240  
 QY 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 300  
 Db 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGG 300  
 QY 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGCCGATTGG 360  
 Db 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGCCGATTGG 360  
 QY 361 TGGAGTAAGGTGTTACGATCGCTCTTATTAGGAAGCAACAGAGCGGTCTGACATGGA 420  
 Db 361 TGGAGTAAGGTGTTACGATCGCTCTTATTAGGAAGCAACAGAGCGGTCTGACATGGA 420  
 QY 421 TTGGACGAACCACTAAATTCGGATTCCGATTCGAGATATTGTTAAGTGCCTAGCTCGATA 480  
 Db 421 TTGGACGAACCACTAAATTCGGATTCCGATTCGAGATATTGTTAAGTGCCTAGCTCGATA 480  
 QY 481 CAATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 481 CTCTRAGAGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523

RESULT 2  
 PCT-US94-06069-1  
 ; Sequence 1, Application PC/TUS9406069  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vical Incorporated  
 ; APPLICANT: Regents of the University of Michigan  
 ; APPLICANT: Nabel, Elizabeth  
 ; APPLICANT: Nabel, Gary  
 ; APPLICANT: Lew, Denise  
 ; APPLICANT: Marquet, Magda  
 ; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear  
 ; STREET: 620 Newport Center Drive 16th Floor  
 ; CITY: Newport Beach  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/06069  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/074,344  
 ; FILING DATE: 07-JUN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Israel, Ned  
 ; REGISTRATION NUMBER: 29,655  
 ; REFERENCE/DOCKET NUMBER: VICAL.033VPC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4965 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: circular  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO

FRAGMENT TYPE:  
ORIGINAL SOURCE:  
STRAIN: HLA-B7 and Beta-2  
PCT-US94-06069-1

Query Match 98.5%; Score 515; DB 5; Length 4965;  
Best Local Similarity 99.0%; Pred. No. 3.9e-174;  
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
DB 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
DB 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
QY 121 CTGCTTCGGATGACGGGCGAGATTCGGGTATCTGAGGGGACTAGGGTGTGTAGG 180  
DB 121 CTGCTTCGGATGACGGGCGAGATTCGGGTATCTGAGGGGACTAGGGTGTGTAGG 180  
QY 181 CGAAAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
DB 181 CGAAAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
QY 301 TAACGATAGTGTAGCAATGCTTACAGGAGGAGAAAGCACCGTCCAGTCCGATGG 360  
DB 301 TAACGATAGTGTAGCAATGCTTACAGGAGGAGAAAGCACCGTCCAGTCCGATGG 360  
QY 361 TGGAGTAAAGTGTGACGATGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420  
DB 361 TGGAGTAAAGTGTGACGATGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420  
QY 421 TTGAGCAACACTTAATTCGCAATTCGAGATGATGATTTAAGTCCCTAGCTCGATA 480  
DB 421 TTGAGCAACACTTAATTCGCAATTCGAGATGATGATTTAAGTCCCTAGCTCGATA 480  
QY 481 CAATAACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
DB 481 CTCTAGACGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523

RESULT 3  
US-08-564-313-2/c  
Sequence 2, Application US/08564313  
Patent No. 5910488  
GENERAL INFORMATION:  
APPLICANT: Nabel, Elizabeth  
APPLICANT: Nabel, Gary  
APPLICANT: Lew, Denise  
APPLICANT: Marcquet, Magda  
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/564,313  
FILING DATE: 01-DEC-1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/074,344  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: VICAL.033CP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4059 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
IMMEDIATE SOURCE:  
CLONE: HLA-B7  
US-08-564-313-2

Query Match 96.7%; Score 505.6; DB 2; Length 4059;  
Best Local Similarity 99.0%; Pred. No. 8.2e-171;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
DB 3415 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 3356  
QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
DB 3355 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 3296  
QY 121 CTGCTTCGGATGACGGGCGAGATTCGGGTATCTGAGGGGACTAGGGTGTGTAGG 180  
DB 3295 CTGCTTCGGATGACGGGCGAGATTCGGGTATCTGAGGGGACTAGGGTGTGTAGG 3236  
QY 181 CGAAAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 240  
DB 3235 CGAAAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTGCG 3176  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 3175 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 3116  
QY 301 TAACGATAGTGTAGCAATGCTTACAGGAGGAGAAAGCACCGTCCAGTCCGATGG 360  
DB 3115 TAACGATAGTGTAGCAATGCTTACAGGAGGAGAAAGCACCGTCCAGTCCGATGG 3056  
QY 361 TGGAGTAAAGTGTGACGATGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420  
DB 3055 TGGAGTAAAGTGTGACGATGCTTATAGGAGGCAACAGACGGGTCTGACATGGA 2996  
QY 421 TTGAGCAACACTAAATTCGCAATTCGAGATGATGATTTAAGTCCCTAGCTCGAT 479  
DB 2995 TTGAGCAACACTAAATTCGCAATTCGAGATGATGATTTAAGTCCCTAGCTCGAT 2936  
QY 480 ACAATAAGGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
DB 2935 ACAATAAGGCCATTGACCAATTCACCAATTTGGTGTGCACCTC 2892

RESULT 4  
PCT-US94-06069-2/c  
Sequence 2, Application PC/TUS9406069  
GENERAL INFORMATION:  
APPLICANT: Nabel, Elizabeth  
APPLICANT: Regente of the University of Michigan  
APPLICANT: Nabel, Elizabeth



Db 261 CGAAAGCGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTAGTTCCG 320  
 QY 241 TTTTGCATAGGAGGGGAAATGCTCTATGCAATCTTGTAGCTTTCGCAATGG 300  
 Db 321 TTTTGCATAGGAGGGGAAATGCTCTATGCAATCTTGTAGCTTTCGCAATGG 380  
 QY 301 TAAGATGATTTAGCAACATGCTTACAGGAGAGAGAAAGACCGTGTGATGCGATTGG 360  
 Db 381 TAAGATGATTTAGCAACATGCTTACAGGAGAGAGAAAGACCGTGTGATGCGATTGG 440  
 QY 361 TGGAGTAAAGTGTACGATCGTCTTATGAGAGGCAACGAGCGGTCTGACATGGA 420  
 Db 441 TGGAGTAAAGTGTACGATCGTCTTATGAGAGGCAACGAGCGGTCTGACATGGA 500  
 QY 421 TTGAGCAACCACTAAATTCGATTCGATTCGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479  
 Db 501 TTGAGCAACCACTAAATTCGATTCGATTCGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 560  
 QY 480 ACAATAAGCCCATTTGACCATTCACCATTTGGTGTGACCTC 523  
 Db 561 ACAATAAGCCCATTTGACCATTCACCATTTGGTGTGACCTC 604

RESULT 6

US-08-235-277-1  
 ; Sequence 1, Application US/08235277  
 ; Patent No. 5733543  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NABEL, GARY J  
 ; APPLICANT: WOFFENDIN, CLIVE  
 ; APPLICANT: YANG, NIN-SUN  
 ; APPLICANT: SHEEHY, MICHAEL J  
 ; TITLE OF INVENTION: INTRODUCTION OF HIV-PROTECTIVE GENES  
 ; TITLE OF INVENTION: INTO CELLS BY PARTICLE-MEDIATED GENE TRANSFER  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/235,277  
 ; FILING DATE: 29-APR-1994  
 ; CLASSIFICATION: 436  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Oblon, No. 5733543man F.  
 ; REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 6042-008-68  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 413-3000  
 ; TELEFAX: (703) 413-2220  
 ; TELEX: 248855 OPAT UR  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5653 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: Other nucleic acid  
 ; US-08-235-277-1

Query Match 96.7%; Score 505.6; DB 1; Length 5653;  
 Best Local Similarity 99.0%; Pred. No. 9,8e-171;  
 Matches 519; Conservative 0; Mismatches 4; Indels 1;

QY 1 CTGCTCCCTGCTTGTGTGCTTGGAGTTCGCTGAGTAGTCCGCGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGCTTGGAGTTCGCTGAGTAGTCCGCGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTCACCGACAATTCGATCAAGAATCTGCTTAGGGTTAGGGGTTTTGGG 120  
 Db 141 ACAAGGCAAGGCTTCACCGACAATTCGATCAAGAATCTGCTTAGGGTTAGGGGTTTTGGG 200  
 QY 121 CTGCTTCGCGATGTACGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 201 CTGCTTCGCGATGTACGGCCAGATATACGCGTATCTGAGGGGACTAGGGTGTGTTAGG 260  
 QY 181 CGAAAGCGGGGCTTCGCTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC 240  
 Db 261 CGAAAGCGGGGCTTCGCTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC 320  
 QY 241 TTTTGCATAGGAGGGGGAATGATGATCTTATGCAATCTCTTGTAGTCTTGCAACATGG 300  
 Db 321 TTTTGCATAGGAGGGGGAATGATGATCTTATGCAATCTCTTGTAGTCTTGCAACATGG 380  
 QY 301 TACGATGATTTAGCAACATGCTTACAGGAGAGAGAAAGACCGTGCATGCCGATGG 360  
 Db 381 TACGATGATTTAGCAACATGCTTACAGGAGAGAGAAAGACCGTGCATGCCGATGG 440  
 QY 361 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACAGACGGGTCTGACATGGA 420  
 Db 441 TGGAGTAAAGTGTACGATCGTCTTATAGGAGGCAACAGACGGGTCTGACATGGA 500  
 QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 479  
 Db 501 TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGATTTAAGTGCCTAGCTCGAT 560  
 QY 480 ACAATAAGCCCATTTGACCATTCACCATTTGGTGTGACCTC 523  
 Db 561 ACAATAAGCCCATTTGACCATTCACCATTTGGTGTGACCTC 604

RESULT 7

US-08-462-859A-6  
 ; Sequence 6, Application US/08462859A  
 ; Patent No. 5652092  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jacobsen, J. S.  
 ; APPLICANT: Vittek, M. P.  
 ; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
 ; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
 ; TITLE OF INVENTION: of B-Amyloid Peptide  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: American Cyanamid Company  
 ; STREET: One Cyanamid Plaza  
 ; CITY: Wayne  
 ; STATE: New Jersey  
 ; COUNTRY: United States  
 ; ZIP: 07470-8426  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/462,859A  
 ; FILING DATE: 05-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Barnhard, Elizabeth M.  
 ; REGISTRATION NUMBER: 31,086  
 ; REFERENCE/DOCKET NUMBER: 31,844-04  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (201)831-3246  
 ; TELEFAX: (201)831-3305  
 ; INFORMATION FOR SEQ ID NO: 6:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3668
US-08-462-859A-6

Query Match          96.7%; Score 505.6; DB 1; Length 8591;
Best Local Similarity 99.0%; Pred. No. 1.2e-170;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTTGGAGGTGCTGAGTAGTGCGGAGCAAAATTTAAGCTACA 60
DB 4716 CTGCTCCCTGCTGTGTTGGAGGTGCTGAGTAGTGCGGAGCAAAATTTAAGCTACA 4775
QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 4835
QY 121 CTGCTTCGCGATGTACGGGCGAGATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180
DB 4836 CTGCTTCGCGATGTACGGGCGAGATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 4895
QY 181 CGAAAGCGGGCTTCGCTGTGACGGGTGAGGAGTCCCTCAGGATATAGTAGTTTCG 240
DB 4896 CGAAAGCGGGCTTCGCTGTGACGGGTGAGGAGTCCCTCAGGATATAGTAGTTTCG 4955
QY 241 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 300
DB 5136 TTTGACGACCACTGAAATTCGCAATTCGAGATATATGTTAAGTGCCTAGCTCGAT 5195
QY 480 ACAATAAGCCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 523
DB 5196 ACAATAAGCCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 5239

RESULT 8
US-08-462-859A-8
; Sequence 8, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3653
US-08-462-859A-8

Query Match          96.7%; Score 505.6; DB 1; Length 8591;
Best Local Similarity 99.0%; Pred. No. 1.2e-170;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTTGGAGGTGCTGAGTAGTGCGGAGCAAAATTTAAGCTACA 60
DB 4716 CTGCTCCCTGCTGTGTTGGAGGTGCTGAGTAGTGCGGAGCAAAATTTAAGCTACA 4775
QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120
DB 4776 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 4835
QY 121 CTGCTTCGCGATGTACGGGCGAGATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180
DB 4836 CTGCTTCGCGATGTACGGGCGAGATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 4895
QY 181 CGAAAGCGGGCTTCGCTGTGACGGGTGAGGAGTCCCTCAGGATATAGTAGTTTCG 240
DB 4896 CGAAAGCGGGCTTCGCTGTGACGGGTGAGGAGTCCCTCAGGATATAGTAGTTTCG 4955
QY 241 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 300
DB 4956 TTTTGCATAGGAGGGGGAATAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 5015
QY 301 TAACGATGATGTACGCAATTCGCTTACAGGAGGAAAGCAACGCTGCATGCCGATTGG 360
DB 5016 TAACGATGATGTACGCAATTCGCTTACAGGAGGAAAGCAACGCTGCATGCCGATTGG 5075
QY 361 TGGAGGTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 5076 TGGAGGTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5135
QY 421 TTGAGCGAACCCTAAATTCGCAATTCGAGATATATGTTAAGTGCCTAGCTCGAT 479
DB 5136 TTTGACGACCACTGAAATTCGCAATTCGAGATATATGTTAAGTGCCTAGCTCGAT 5195
QY 480 ACAATAAGCCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 523
DB 5196 ACAATAAGCCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 5239

RESULT 9
US-08-123-659A-6
; Sequence 6, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.

```

```

; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3868
; US-08-123-659A-6

Query Match 96.7%; Score 505.6; DB 1; Length 8591;
Best Local Similarity 99.0%; Pred. No. 1.2e-170;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTAGTGGCGAGCAAAATTAAGTACA 60
Db 4716 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTAGTGGCGAGCAAAATTAAGTACA 4775
Qy 61 ACAAGGCAAGGCTTGCACGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCG 120
Db 4776 ACAAGGCAAGGCTTGCACGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCG 4835
Qy 121 CTGCTTCGCGATGACGGGCGCAGATATTCGGTATCTGAGGGGACTAGGCTGTCTTAGG 180
Db 4836 CTGCTTCGCGATGACGGGCGCAGATATTCGGTATCTGAGGGGACTAGGCTGTCTTAGG 4895
Qy 181 CGAAAACGGGGCTTCGGTGTGTAGAGTCCCTCAGGATATAGTAGTTTCG 240
Db 4896 CGAAAACGGGGCTTCGGTGTGTAGAGTCCCTCAGGATATAGTAGTTTCG 4955
Qy 241 TTTTGTATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
Db 4956 TTTTGTATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015
Qy 301 TAACGATGATGATGACATGCTCTTACAAGGAGGAAAGACCGTGCATGCCGATTCG 360
Db 5016 TAACGATGATGATGACATGCTCTTACAAGGAGGAAAGACCGTGCATGCCGATTCG 5075
Qy 361 TGGAGTAAAGTGTGACGATCGTSCCTTTATAGGAGGCAACACGCGGTCTGACATGA 420
Db 5076 TGGAGTAAAGTGTGACGATCGTSCCTTTATAGGAGGCAACACGCGGTCTGACATGA 5135
Qy 421 TTGAGCGAACCACTAAATTCGGATTTGGAGAGAT-ATTGTATTTAAGTGCCTAGTTCGAT 479

```

```

Db 5136 TTGGAGCAACCACTGAATTCGGATTCGAGAGATAATTTAAGTCCCTAGTCCGAT 5195
Qy 480 ACAATTAAGCCATTGACCATTCACCATTCACCATTCGTTGGTGCACCTC 523
Db 5196 ACAATAAAGCCATTGACCATTCACCATTCACCATTCGTTGGTGCACCTC 5239

RESULT 10
US-08-123-659A-8
; Sequence 8, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
; US-08-123-659A-8

Query Match 96.7%; Score 505.6; DB 1; Length 8591;
Best Local Similarity 99.0%; Pred. No. 1.2e-170;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTAGTGGCGAGCAAAATTAAGTACA 60
Db 4716 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTAGTGGCGAGCAAAATTAAGTACA 4775
Qy 61 ACAAGGCAAGGCTTGCACGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCG 120
Db 4776 ACAAGGCAAGGCTTGCACGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCG 4835
Qy 121 CTGCTTCGCGATGACGGGCGCAGATATTCGGTATCTGAGGGGACTAGGCTGTCTTAGG 180
Db 4836 CTGCTTCGCGATGACGGGCGCAGATATTCGGTATCTGAGGGGACTAGGCTGTCTTAGG 4895
Qy 181 CGAAAACGGGGCTTCGGTGTGTAGAGTCCCTCAGGATATAGTAGTTTCG 240
Db 4896 CGAAAACGGGGCTTCGGTGTGTAGAGTCCCTCAGGATATAGTAGTTTCG 4955

```

QY 241 TTTTTCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTGTAGTCTTGCACATGG 300  
Db 4956 TTTTTCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTGTAGTCTTGCACATGG 5015  
QY 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 360  
Db 5016 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 5075  
QY 361 TGGAAAGTAAGTGTAGTACGATGCTTATGCAATACTCTGTAGTCTTGCACATGG 420  
Db 5076 TGGAAAGTAAGTGTAGTACGATGCTTATGCAATACTCTGTAGTCTTGCACATGG 5135  
QY 421 TTTGAGCAACCACTAAATTCGCGATTCAGAGAT -ATTGTATTAAAGTCCCTAGTCCGAT 479  
Db 5136 TTTGAGCAACCACTAAATTCGCGATTCAGAGAT -ATTGTATTAAAGTCCCTAGTCCGAT 5195  
QY 480 ACAATAAACGCCATTGGACCATTCACCAATTTGGTGTGCACCTC 523  
Db 5196 ACAATAAACGCCATTGGACCATTCACCAATTTGGTGTGCACCTC 5239

## RESULT 11

US-08-464-247A-6  
; Sequence 6, Application US/08464247A  
; Patent No. 5693478  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vitek, M. P.  
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
; TITLE OF INVENTION: of B-Amyloid Peptide  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,844-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-683-2158  
; TELEFAX: 201-683-4117  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8591 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 2393...3868  
US-08-464-247A-6

Query Match 36.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGAGGTCGCTGAGTGTGCGAGCAAAATTTAAAGCTACA 60  
|||||

Db 4716 CTGCTCCCTGCTGTGTGAGGTCGCTGAGTGTGCGAGCAAAATTTAAAGCTACA 4775  
QY 61 ACAGGCAAGGCTTGACCCACAAATTTGCATCAAGAAATCTGCTTAGGGTTAGGCGTTTCGG 120  
Db 4776 ACAGGCAAGGCTTGACCCACAAATTTGCATCAAGAAATCTGCTTAGGGTTAGGCGTTTCGG 4835  
QY 121 CTGCTTCGCGATGTACGGCCAGATATTTCGCGTATCTGAGGGGACTAGGGTGTGTTTAGG 180  
Db 4836 CTGCTTCGCGATGTACGGCCAGATATTTCGCGTATCTGAGGGGACTAGGGTGTGTTTAGG 4895  
QY 181 CGAAAAGCGGGGCTTCGTTGTGACGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240  
Db 4896 CGAAAAGCGGGGCTTCGTTGTGACGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 4955  
QY 241 TTTTTCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTGTAGTCTTGCACATGG 300  
Db 4956 TTTTTCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTGTAGTCTTGCACATGG 5015  
QY 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 360  
Db 5016 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 5075  
QY 361 TGGAAAGTAAGTGTAGTACGATGCTTATGCAATACTCTGTAGTCTTGCACATGG 420  
Db 5076 TGGAAAGTAAGTGTAGTACGATGCTTATGCAATACTCTGTAGTCTTGCACATGG 5135  
QY 421 TTTGAGCAACCACTAAATTCGCGATTCAGAGAT -ATTGTATTAAAGTCCCTAGTCCGAT 479  
Db 5136 TTTGAGCAACCACTAAATTCGCGATTCAGAGAT -ATTGTATTAAAGTCCCTAGTCCGAT 5195  
QY 480 ACAATAAACGCCATTGGACCATTCACCAATTTGGTGTGCACCTC 523  
Db 5196 ACAATAAACGCCATTGGACCATTCACCAATTTGGTGTGCACCTC 5239

## RESULT 12

US-08-464-247A-8  
; Sequence 8, Application US/08464247A  
; Patent No. 5693478  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vitek, M. P.  
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
; TITLE OF INVENTION: of B-Amyloid Peptide  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,844-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-683-2158  
; TELEFAX: 201-683-4117  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8591 base pairs  
; TYPE: nucleic acid



STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2393...3853  
US-08-464-247A-8

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 4716 CTGCTCCCTGCTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 4775  
QY 61 ACAAGGCAAGGCTTGACGCAATTCATGAAGATCTGCTTAGGGCTTAGGGCTTTTGG 120  
Db 4776 ACAAGGCAAGGCTTGACGCAATTCATGAAGATCTGCTTAGGGCTTAGGGCTTTTGG 4835  
QY 121 CTGCTTCGCGATGTCAGGCGCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGTCAGGCGCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTAGG 4895  
QY 181 CGAAAACGGGGCTTCGGTCTGTCAGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 240  
Db 4896 CGAAAACGGGGCTTCGGTCTGTCAGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 4955  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
Db 5136 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 5195  
QY 480 ACAATAAGCCATTGACCATTCACCATTTGGTGTGTCACCTC 523  
Db 5196 ACAATAAGCCATTGACCATTCACCATTTGGTGTGTCACCTC 5239

## RESULT 13

US-08-464-248A-6  
Sequence 6, Application US/08464248A  
Patent No. 5703209

GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.  
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2393...3868  
US-08-464-248A-6

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 4716 CTGCTCCCTGCTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 4775  
QY 61 ACAAGGCAAGGCTTGACGCAATTCATGAAGATCTGCTTAGGGCTTAGGGCTTTTGG 120  
Db 4776 ACAAGGCAAGGCTTGACGCAATTCATGAAGATCTGCTTAGGGCTTAGGGCTTTTGG 4835  
QY 121 CTGCTTCGCGATGTCAGGCGCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTAGG 180  
Db 4836 CTGCTTCGCGATGTCAGGCGCAGATATTCGCTATCTGAGGGACTAGGGTGTGTTAGG 4895  
QY 181 CGAAAACGGGGCTTCGGTCTGTCAGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 240  
Db 4896 CGAAAACGGGGCTTCGGTCTGTCAGGGTTAGGAGTCCCTCAGGATATAGTGTTCGC 4955  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
Db 4956 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTTGTAGTCTTGCACATGG 5015  
QY 301 TACGATGAGTGTAGCAACATGCTTCAAGGAGAGAAAGACCCGTGATGCCGATGG 360  
Db 5016 TACGATGAGTGTAGCAACATGCTTCAAGGAGAGAAAGACCCGTGATGCCGATGG 5075  
QY 361 TGGAAAGTAAGTGTGTCAGTCTGTCCTTATAGGAAGCAACAGAGGGTCTGACATGGA 420  
Db 5076 TGGAAAGTAAGTGTGTCAGTCTGTCCTTATAGGAAGCAACAGAGGGTCTGACATGGA 5135  
QY 421 TTGACCAACCACTAAATTCGGATTTGCAGAGAT-ATTGTAATTAAGTSCCTAGCTCCAT 479  
Db 5136 TTGACCAACCACTAAATTCGGATTTGCAGAGAT-ATTGTAATTAAGTSCCTAGCTCCAT 5195  
QY 480 ACAATAAGCCATTGACCATTCACCATTTGGTGTGTCACCTC 523  
Db 5196 ACAATAAGCCATTGACCATTCACCATTTGGTGTGTCACCTC 5239

## RESULT 14

US-08-464-248A-8  
Sequence 8, Application US/08464248A  
Patent No. 5703209

GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.  
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2393..3853  
US-08-464-248A-8

Query Match 96.7%; Score 505.6; DB 1; Length 8591;  
Best Local Similarity 99.0%; Pred. No. 1.2e-170;  
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTCTGTGTGTGGAGTCTGCTGAGTGTGCGCGAGCAAAATTTAAGCTACA 60  
DB 4716 CTGCTCCCTCTGTGTGTGGAGTCTGCTGAGTGTGCGCGAGCAAAATTTAAGCTACA 4775  
QY 61 ACAAGGCAAGCTTGACCGCAATTCGATGAAGATCTGCTTAGGTTAGGCGTTTTCG 120  
DB 4776 ACAAGGCAAGCTTGACCGCAATTCGATGAAGATCTGCTTAGGTTAGGCGTTTTCG 4835  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTAGG 180  
DB 4836 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTAGG 4895  
QY 181 CGAAAAGCGGGGCTTCGGTTTACCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCG 240  
DB 4896 CGAAAAGCGGGGCTTCGGTTTACCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCG 4955  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 4956 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 5015  
QY 301 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGCAACCGCTGCATGCCGATTGG 360  
DB 5016 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGCAACCGCTGCATGCCGATTGG 5075  
QY 361 TGGAGTAAAGTGGTACGATCGTCCCTTATTAGGAAGCAACAGACGGCTCTGACATGGA 420  
DB 5076 TGGAGTAAAGTGGTACGATCGTCCCTTATTAGGAAGCAACAGACGGCTCTGACATGGA 5135  
QY 421 TTGGACGACCACTAAATTCGGATTCAGAGAT-ATTGTATTATAGTCCCTAGCTCGAT 479  
DB 5136 TTGGACGACCACTAAATTCGGATTCAGAGAT-ATTGTATTATAGTCCCTAGCTCGAT 5195  
QY 480 ACAATAAAGCCCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 523

DB 5196 ACAATAAAGCCCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 5239  
RESULT 15  
US-09-479-122-18  
Sequence 18, Application US/09479122  
Patent No. 6410266  
GENERAL INFORMATION:  
APPLICANT: HARRINGTON, JOHN J.  
APPLICANT: SHERF, BRUCE  
APPLICANT: RUNDLETT, STEPHEN  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
FILE OF INVENTION: ENDOGENOUS GENES  
FILE REFERENCE: 0221-0003C  
CURRENT APPLICATION NUMBER: US/09/479,122  
CURRENT FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: 09/276,820  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 09/159,643  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 08/941,223  
PRIOR FILING DATE: 1997-09-26  
PRIOR APPLICATION NUMBER: 09/263,814  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: 09/253,022  
PRIOR FILING DATE: 1999-02-19  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 18  
LENGTH: 6836  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-479-122-18

Query Match 95.8%; Score 500.8; DB 4; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 5.8e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTCTGTGTGTGGAGTCTGCTGAGTGTGCGCGAGCAAAATTTAAGCTACA 60  
DB 1299 CTGCTCCCTCTGTGTGTGGAGTCTGCTGAGTGTGCGCGAGCAAAATTTAAGCTACA 1358  
QY 61 ACAAGGCAAGCTTGACCGCAATTCGATGAAGATCTGCTTAGGTTAGGCGTTTTCG 120  
DB 1359 ACAAGGCAAGCTTGACCGCAATTCGATGAAGATCTGCTTAGGTTAGGCGTTTTCG 1418  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTAGG 180  
DB 1419 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTAGG 1478  
QY 181 CGAAAAGCGGGGCTTCGGTTTACCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCG 240  
DB 1479 CGCCCAGCGGGGCTTCGGTTTACCGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCG 1538  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
DB 1539 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1598  
QY 301 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGCAACCGCTGCATGCCGATTGG 360  
DB 1599 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAAGCAACCGCTGCATGCCGATTGG 1658  
QY 361 TGGAGTAAAGTGGTACGATCGTCCCTTATTAGGAAGCAACAGACGGCTCTGACATGGA 420  
DB 1659 TGGAGTAAAGTGGTACGATCGTCCCTTATTAGGAAGCAACAGACGGCTCTGACATGGA 1718  
QY 421 TTGGACGACCACTAAATTCGGATTCAGAGAT-ATTGTATTATAGTCCCTAGCTCGAT 479  
DB 1719 TTGGACGACCACTAAATTCGGATTCAGAGAT-ATTGTATTATAGTCCCTAGCTCGAT 1778  
QY 480 ACAATAAAGCCCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 523

Db 1779 ACAATAAACGCCATTGACCAATTGACCAATTGCGTGTGCACCTC 1822

## RESULT 16

US-09-484-997-18  
; Sequence 18, Application US/09484997  
; Patent No. 6524818  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003J  
; CURRENT APPLICATION NUMBER: US/09/484,997  
; CURRENT FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6836  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-484-997-18

Query Match 95.8%; Score 500.8; DB 4; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 5.8e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTGTGCGGAGCAAAATTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTGTGCGGAGCAAAATTAAGCTACA 1358  
QY 61 ACAAGGCAAGGCTTGACGCGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 120  
Db 1359 ACAAGGCAAGGCTTGACGCGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 1418  
QY 121 CTGCTCCGATGTACGCGGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 180  
Db 1419 CTGCTCCGATGTACGCGGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 1478  
QY 181 CGAAAAGCGGGCTTCGGTGTGTACGCGGTTAGGATCCCTCAGGATATAGTATGCTTCGC 240  
Db 1479 CGCCAGCGGGCTTCGGTGTGTACGCGGTTAGGATCCCTCAGGATATAGTATGCTTCGC 1538  
QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 1539 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1598  
QY 301 TAACGATGAGTTAGCAATGCCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
Db 1599 TAACGATGAGTTAGCAATGCCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1658  
QY 361 TGGAGTAAAGTGTGATGATCGTGTCTTATAGGAGGCAACAGACGGGTCTGACATGA 420  
Db 1659 TGGAGTAAAGTGTGATGATCGTGTCTTATAGGAGGCAACAGACGGGTCTGACATGA 1718  
QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAGTGTGCTAGCTCGAT 479  
Db 1719 TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAGTGTGCTAGCTCGAT 1778  
QY 480 ACAATAAACGCCATTGACCAATTGACCAATTGCGTGTGCACCTC 523  
Db 1779 ACAATAAACGCCATTGACCAATTGACCAATTGCGTGTGCACCTC 1822

## RESULT 17

US-09-481-355-18  
; Sequence 18, Application US/09481355  
; Patent No. 6524824  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003F  
; CURRENT APPLICATION NUMBER: US/09/481,355  
; CURRENT FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6836  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-481-355-18

Query Match 95.8%; Score 500.8; DB 4; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 5.8e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTGTGCGGAGCAAAATTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTGTGCGGAGCAAAATTAAGCTACA 1358  
QY 61 ACAAGGCAAGGCTTGACGCGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 120  
Db 1359 ACAAGGCAAGGCTTGACGCGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 1418  
QY 121 CTGCTCCGATGTACGCGGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 180  
Db 1419 CTGCTCCGATGTACGCGGCAATTCATGAAGATCTGTTAGGGGACTAGGGTGTGTTAGG 1478  
QY 181 CGAAAAGCGGGCTTCGGTGTGTACGCGGTTAGGATCCCTCAGGATATAGTATGCTTCGC 240  
Db 1479 CGCCAGCGGGCTTCGGTGTGTACGCGGTTAGGATCCCTCAGGATATAGTATGCTTCGC 1538  
QY 241 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 1539 TTTTGCATAGGAGGGGAAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1598  
QY 301 TAACGATGAGTTAGCAATGCCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 360  
Db 1599 TAACGATGAGTTAGCAATGCCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGG 1658  
QY 361 TGGAGTAAAGTGTGATGATCGTGTCTTATAGGAGGCAACAGACGGGTCTGACATGA 420  
Db 1659 TGGAGTAAAGTGTGATGATCGTGTCTTATAGGAGGCAACAGACGGGTCTGACATGA 1718  
QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAGTGTGCTAGCTCGAT 479  
Db 1719 TTGAGCAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAGTGTGCTAGCTCGAT 1778  
QY 480 ACAATAAACGCCATTGACCAATTGACCAATTGCGTGTGCACCTC 523  
Db 1779 ACAATAAACGCCATTGACCAATTGACCAATTGCGTGTGCACCTC 1822



```

; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERE, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-479-123-18

Query Match          95.8%; Score 500.8; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No.5.8e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1

QY 1 CTGCTCCCTGCTGTGTGTGTGGAGGTGCGCTAGTAGTGTGCGCGAGCAAAATTTAAGCTACA 60
Db 1299 CTGCTCCCTGCTGTGTGTGTGGAGTGCCTAGTAGTGTGCGCGAGCAAAATTTAAGCTACA 1358

QY 61 ACAAGCGAGGCTTGACCGACAATTGCAAGAATACTGCTTHAGGGTTAGCGGTTTTGGC 120
Db 1359 ACAAGCGAAGCTTGACCGACAATTGCAATGAAGAATCTGCTTAGGGTTAGCGGTTTTGGC 1418

QY 121 CTGCTTCCGCGATGTACGGGCCAGATAATTGCGCTATCTTGAGGGGACTAGGGGTGTGTTAGG 180
Db 1419 CTGCTTCCGCGATGTACGGGCCAGATAATACGCGTATCTTGAGGGGACTACGGGTGTGTTAGG 1478

QY 181 CGAAAAGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGC 240
Db 1479 CGCCACAGCGGGGTTTCGGTTGTACGCGGTTAGAGTCCCTCAGATATAGTAGTTTCGC 1538

QY 241 TTTTCGATAGGAGGGGGAAATGTAAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATCG 300
Db 1539 TTTTCGATAGGAGGGGGAAATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATCG 1598

QY 301 TTAACGATGTTAGCAACATGCTCTTACAGGAGAGAAAGACACGTCGATGCCGATTGG 360
Db 1599 TTAACGATGTTAGCAACATGCTCTTACAGGAGAGAAAGACACGTCGATGCCGATTGG 1658

QY 361 TGGAAAGTAAGTGCTGACGATCGTGCTCTTATTAGGAGGCAACAAGCGGCTCGACATGGA 420
Db 1659 TGGAAAGTAAGTGCTGACGATCGTGCTCTTATTAGGAGGCAACAAGCGGCTCGACATGGA 1718

QY 421 TTGGACGAACCACTAAATTCGCAATTGCGAGAT-ATTGTATTAAAGTGCTAGCTCGAT 479
Db 1719 TTGGACGAACCACTGAAATTCGCAATTGCGAGATAATTGTAATTAAAGTGCTAGCTCGAT 1778

QY 480 ACAATAACGGCAATTGACCAATTCACCAATTTGTTGTGCACTC 523
Db 1779 ACAATAACGGCAATTGACCAATTCACCAATTTGTTGTGCACTC 1822

```

RESULT 21  
US-09-479-123-18  
; Sequence 18, Application US/09479123  
; Patent No. 6670185

```

; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-22

```

```

Query Match 95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGTGGAGGTGCGTGTAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGTGTGGAGGTGCGTGTAGTGTGCGGAGCAAAATTTAAGCTACA 1211
QY 61 ACAAGGCAAGGCTTGACGCAAAATTCATGAAGAATCTGTTAGGTTAGGCGTTTGGG 120
DB 1212 ACAAGGCAAGGCTTGACGCAAAATTCATGAAGAATCTGTTAGGTTAGGCGTTTGGG 1271
QY 121 CTGCTTCGCGATGTACGCGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTAGG 180
DB 1272 CTGCTTCGCGATGTACGCGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTAGG 1331
QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTTGGC 240
DB 1332 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTTGGC 1391
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
DB 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451
QY 301 TAACGATGATGTAGCAACATGCTTACAAGGAGAAAGAACCCGTCGATGCCGATTGG 360
DB 1452 TAACGATGATGTAGCAACATGCTTACAAGGAGAAAGAACCCGTCGATGCCGATTGG 1511
QY 361 TGGAGTAAAGGTGTAGTATGCTGCTTATTTAGGAGGCAACAGACGGTCTGACATGA 420
DB 1512 TGGAGTAAAGGTGTAGTATGCTGCTTATTTAGGAGGCAACAGACGGTCTGACATGA 1571
QY 421 TTGACGAAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479
DB 1572 TTGACGAAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631
QY 480 ACAATTAAGCCATTTGACATTCACACATATGTTGTGTGCACCTC 523
DB 1632 ACAATTAAGCCATTTGACATTCACACATATGTTGTGTGCACCTC 1675

```

RESULT 23

```

US-09-479-122-23
; Sequence 23, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTGTGGAGGTGCGTGTAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGTGTGGAGGTGCGTGTAGTGTGCGGAGCAAAATTTAAGCTACA 1211
QY 61 ACAAGGCAAGGCTTGACGCAAAATTCATGAAGAATCTGTTAGGTTAGGCGTTTGGG 120
DB 1212 ACAAGGCAAGGCTTGACGCAAAATTCATGAAGAATCTGTTAGGTTAGGCGTTTGGG 1271
QY 121 CTGCTTCGCGATGTACGCGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTAGG 180
DB 1272 CTGCTTCGCGATGTACGCGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTAGG 1331
QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTTGGC 240
DB 1332 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATGCTTGGC 1391
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
DB 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451
QY 301 TAACGATGATGTAGCAACATGCTTACAAGGAGAAAGAACCCGTCGATGCCGATTGG 360
DB 1452 TAACGATGATGTAGCAACATGCTTACAAGGAGAAAGAACCCGTCGATGCCGATTGG 1511
QY 361 TGGAGTAAAGGTGTAGTATGCTGCTTATTTAGGAGGCAACAGACGGTCTGACATGA 420
DB 1512 TGGAGTAAAGGTGTAGTATGCTGCTTATTTAGGAGGCAACAGACGGTCTGACATGA 1571
QY 421 TTGACGAAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479
DB 1572 TTGACGAAACCACTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631

```

\_\_\_\_\_

Db 1392 TTTGCTAGGGAGGGGAAATGTA

361 TGGAAAGTAAGGTGGTACGATCGTGCCTTATTAGGAAGCAACAGACGGGCTGACATGGA 420

Qy 61 ACAAGCAGGCTTGACCGACAAATCGATGAAGAATCTGCTTAGGCTTAGCGTTTTCG 120  
Db 1212 ACAAGCAGGCTTGACCGACAAATGCAATGCAATCTGCTTAGGCTTAGCGTTTTCG 1271

181 CGAAAAGCGGGGCTTCGGTGTACGGGTAGGAGTCCCTCAGGATATAGTA





```

Query Match      95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTCTGTTGTTGAGAGTCTGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTCTGTTGTTGAGAGTCTGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 1211
QY 61 ACAAGGCAAGGCTTGACCGACAATTTGATGATGAAGAATCTGTTAGGCTTAGGCGTTTTCGG 120
DB 1212 ACAAGGCAAGGCTTGACCGACAATTTGATGATGAAGAATCTGTTAGGCTTAGGCGTTTTCGG 1271
QY 121 CTGCTTCGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 180
DB 1272 CTGCTTCGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 1331
QY 181 CGAAAGCGGGGCTTCGGTTGATGCGGTTAGGAGTCCCTCAGGATATAGTATTCGC 240
DB 1332 CGCCAGCGGGGCTTCGGTTGATGCGGTTAGGAGTCCCTCAGGATATAGTATTCGC 1391
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTTATGCAATACTTGTAGTCTTGCAACATGG 300
DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTTATGCAATACTTGTAGTCTTGCAACATGG 1451
QY 301 TAAAGTAGTGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 360
DB 1452 TAAAGTAGTGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 1511
QY 361 TGAAGTAGTGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 420
DB 1512 TGAAGTAGTGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 1571
QY 421 TTGACGAAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479
DB 1572 TTGACGAAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 1631
QY 480 ACAATAAGCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 523
DB 1632 ACAATAAGCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 1675

```

```

RESULT 30
US-09-481-355-28
; Sequence 28, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)

```

```

; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-28

Query Match      95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTCTGTTGTTGAGAGTCTGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTCTGTTGTTGAGAGTCTGCTGAGTAGTGTGCGGAGCAAAATTTAAGCTACA 1211
QY 61 ACAAGGCAAGGCTTGACCGACAATTTGATGATGAAGAATCTGTTAGGCTTAGGCGTTTTCGG 120
DB 1212 ACAAGGCAAGGCTTGACCGACAATTTGATGATGAAGAATCTGTTAGGCTTAGGCGTTTTCGG 1271
QY 121 CTGCTTCGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 180
DB 1272 CTGCTTCGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 1331
QY 181 CGAAAGCGGGGCTTCGGTTGATGCGGTTAGGAGTCCCTCAGGATATAGTATTCGC 240
DB 1332 CGCCAGCGGGGCTTCGGTTGATGCGGTTAGGAGTCCCTCAGGATATAGTATTCGC 1391
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTTATGCAATACTTGTAGTCTTGCAACATGG 300
DB 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTTATGCAATACTTGTAGTCTTGCAACATGG 1451
QY 301 TAAAGTAGTGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 360
DB 1452 TAAAGTAGTGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 1511
QY 361 TGAAGTAGTGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 420
DB 1512 TGAAGTAGTGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATGG 1571
QY 421 TTGACGAAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 479
DB 1572 TTGACGAAACCACTAAATTCGCAATTCGAGAGAT-ATTGTATTTAAGTCCCTAGCTCGAT 1631
QY 480 ACAATAAGCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 523
DB 1632 ACAATAAGCCATTTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 31
US-09-481-282-22
; Sequence 22, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA

```

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (8347)  
OTHER INFORMATION: a, c, t, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (8499)  
OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-481-282-22

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db 1152 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 1211
QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTTGCG 120
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTTGCG 1271
QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCGTATCTGAGGGGAATAGGGTGTGTTAGG 180
Db 1272 CTGCTTCGCGATGACGGGCCAGATATTCGCGTATCTGAGGGGAATAGGGTGTGTTAGG 1331
QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 240
Db 1332 CGCCACGGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 1391
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
Db 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451
QY 301 TAACGATGAGTTAGCAATGCGCTTACAAGGAGAGAAAAGCACCGTGCATGCGATTGG 360
Db 1452 TAACGATGAGTTAGCAATGCGCTTACAAGGAGAGAAAAGCACCGTGCATGCGATTGG 1511
QY 361 TGGAGTAAAGTGTGATGATGCTGCTTATAGGAGGCAACAGACGGGTCTGACATGA 420
Db 1512 TGGAGTAAAGTGTGATGATGCTGCTTATAGGAGGCAACAGACGGGTCTGACATGA 1571
QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479
Db 1572 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631
QY 480 ACAATAAGCGCAATTCACCAATTCACCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 523
Db 1632 ACAATAAGCGCAATTCACCAATTCACCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1675
```

## RESULT 32

US-09-481-282-23  
Sequence 23, Application US/09481282  
Patent No. 6541221

GENERAL INFORMATION:  
APPLICANT: HARRINGTON, JOHN J.  
APPLICANT: SHERF, BRUCE  
APPLICANT: RUNDLETT, STEPHEN  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
FILE REFERENCE: 0221-0003US  
CURRENT APPLICATION NUMBER: US/09/481,282  
PRIOR APPLICATION NUMBER: 09/159,643  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 08/941,223  
PRIOR FILING DATE: 1997-09-26  
PRIOR APPLICATION NUMBER: 09/263,814  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: 09/253,022  
PRIOR FILING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23  
LENGTH: 9737  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (8347)  
OTHER INFORMATION: a, c, t, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (8499)  
OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-481-282-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db 1152 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 1211
QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTTGCG 120
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTTGCG 1271
QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCGTATCTGAGGGGAATAGGGTGTGTTAGG 180
Db 1272 CTGCTTCGCGATGACGGGCCAGATATTCGCGTATCTGAGGGGAATAGGGTGTGTTAGG 1331
QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 240
Db 1332 CGCCACGGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTATTGCG 1391
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
Db 1392 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451
QY 301 TAACGATGAGTTAGCAATGCGCTTACAAGGAGAGAAAAGCACCGTGCATGCGATTGG 360
Db 1452 TAACGATGAGTTAGCAATGCGCTTACAAGGAGAGAAAAGCACCGTGCATGCGATTGG 1511
QY 361 TGGAGTAAAGTGTGATGATGCTGCTTATAGGAGGCAACAGACGGGTCTGACATGA 420
Db 1512 TGGAGTAAAGTGTGATGATGCTGCTTATAGGAGGCAACAGACGGGTCTGACATGA 1571
QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479
Db 1572 TTGAGCAACCACTAAATTCGCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1631
QY 480 ACAATAAGCGCAATTCACCAATTCACCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 523
Db 1632 ACAATAAGCGCAATTCACCAATTCACCAATTCGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1675
```

## RESULT 33

US-09-481-282-28  
Sequence 28, Application US/09481282  
Patent No. 6541221

GENERAL INFORMATION:  
APPLICANT: HARRINGTON, JOHN J.  
APPLICANT: SHERF, BRUCE  
APPLICANT: RUNDLETT, STEPHEN  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
FILE REFERENCE: 0221-0003US  
CURRENT APPLICATION NUMBER: US/09/481,282  
CURRENT FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 09/159,643  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 08/941,223

```

; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; TYPE: DNA
; LENGTH: 9737
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-28

Query Match          95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGCAGCAAAATTTAAGCTACA 1211

QY 61 ACAAGCAGAGCTTGACCGCAATTCGATGAGTAGTGCAGCAAAATTTAAGCTACA 120
DB 1212 ACAAGCAGAGCTTGACCGCAATTCGATGAGTAGTGCAGCAAAATTTAAGCTACA 1271

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180
DB 1272 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 1331

QY 181 CGAAAGCGGGCTTCGCGTGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 240
DB 1332 CGCGCCAGCGGGCTTCGCGTGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 1391

QY 241 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGG 300
DB 1392 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGG 1451

QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 360
DB 1452 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 1511

QY 361 TGAAGTAAGTGTAGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGGCTGCACATGGA 420
DB 1512 TGAAGTAAGTGTAGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGGCTGCACATGGA 1571

QY 421 TTGGAGCAACACCTAAATTCGCGATTCGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 479
DB 1572 TTGGAGCAACACCTAAATTCGCGATTCGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 1631

QY 480 ACAATAAGCGCATTTGACCATTCACCAATTCGCGATTCGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 523
DB 1632 ACAATAAGCGCATTTGACCATTCACCAATTCGCGATTCGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 1675

```

```

RESULT 34
US-09-455-659A-22
; Sequence 22, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERE, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003A

```

```

; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

Query Match          95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTGTGTGGAGGTGCTGAGTAGTGCAGCAAAATTTAAGCTACA 1211

QY 61 ACAAGCAGAGCTTGACCGCAATTCGATGAGTAGTGCAGCAAAATTTAAGCTACA 120
DB 1212 ACAAGCAGAGCTTGACCGCAATTCGATGAGTAGTGCAGCAAAATTTAAGCTACA 1271

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180
DB 1272 CTGCTTCGCGATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 1331

QY 181 CGAAAGCGGGCTTCGCGTGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 240
DB 1332 CGCGCCAGCGGGCTTCGCGTGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 1391

QY 241 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGG 300
DB 1392 TTTTGCATAGGAGGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGG 1451

QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 360
DB 1452 TAACGATGAGTTAGCAACATGCTTACAGGAGGAGAAAGCAACCGTGCATGCCGATTGG 1511

QY 361 TGAAGTAAGTGTAGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGGCTGCACATGGA 420
DB 1512 TGAAGTAAGTGTAGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGGCTGCACATGGA 1571

QY 421 TTGGAGCAACACCTAAATTCGCGATTCGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 479
DB 1572 TTGGAGCAACACCTAAATTCGCGATTCGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 1631

QY 480 ACAATAAGCGCATTTGACCATTCACCAATTCGCGATTCGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 523
DB 1632 ACAATAAGCGCATTTGACCATTCACCAATTCGCGATTCGAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGAT 1675

```

```

RESULT 35
US-09-455-659A-23
; Sequence 23, Application US/09455659A
; Patent No. 6602686

```

GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003A  
; CURRENT APPLICATION NUMBER: US/09/455,659A  
; CURRENT FILING DATE: 1999-12-07  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 9737  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8347)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8499)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-455-659A-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 1211  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAAATCTGTTAGGGTTAGCGGTTTGGG 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAAATCTGTTAGGGTTAGCGGTTTGGG 1271  
QY 121 CTGCTTCGCGATGTACGGGCGCAGATATTCGCGTATCTGAGGGGACTAGGGTGTCTTAGG 180  
Db 1272 CTGCTTCGCGATGTACGGGCGCAGATATTCGCGTATCTGAGGGGACTAGGGTGTCTTAGG 1331  
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 240  
Db 1332 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 1391  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451  
QY 301 TAACGATGATGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 360  
Db 1452 TAACGATGATGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 1511  
QY 361 TGGAGTAAAGTGTAGTACGTCGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
Db 1512 TGGAGTAAAGTGTAGTACGTCGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 1571  
QY 421 TTGAGCAACACCTAATTCGATTCGATTCGAGAT-ATTGTATTAAATGTCCTAGCTCGAT 479  
Db 1572 TTGAGCAACACCTAATTCGATTCGATTCGAGAT-ATTGTATTAAATGTCCTAGCTCGAT 1631  
QY 480 ACAATAAGCGCATTTGACCATTCACCATTTGGTGTGCACTC 523  
|||||

Db 1632 ACAATAAGCGCATTTGACCATTCACCATTTGGTGTGCACTC 1675  
RESULT 36  
US-09-455-659A-28  
; Sequence 28, Application US/09455659A  
; Patent No. 6602686  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003A  
; CURRENT APPLICATION NUMBER: US/09/455,659A  
; CURRENT FILING DATE: 1999-12-07  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 9737  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8347)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8499)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-455-659A-28

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 1152 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 1211  
QY 61 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAAATCTGTTAGGGTTAGCGGTTTGGG 120  
Db 1212 ACAAGGCAAGGCTTGACCGCAATTCGATGAAGAAATCTGTTAGGGTTAGCGGTTTGGG 1271  
QY 121 CTGCTTCGCGATGTACGGGCGCAGATATTCGCGTATCTGAGGGGACTAGGGTGTCTTAGG 180  
Db 1272 CTGCTTCGCGATGTACGGGCGCAGATATTCGCGTATCTGAGGGGACTAGGGTGTCTTAGG 1331  
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 240  
Db 1332 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCG 1391  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
Db 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451  
QY 301 TAACGATGATGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 360  
Db 1452 TAACGATGATGTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCGATTGG 1511  
QY 361 TGGAGTAAAGTGTAGTACGTCGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 420  
Db 1512 TGGAGTAAAGTGTAGTACGTCGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGA 1571

QY 421 TTGGACGAACCACTAAATTCGGATTGCGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 479  
 Db 1572 TTGGACGAACCACTAAATTCGGATTGCGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 1631  
 QY 480 ACAATAAGCCCAATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 1632 ACAATAAGCCCAATTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 37  
 US-09-484-996-22  
 ; Sequence 22, Application US/09484996  
 ; Patent No. 6623958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003H  
 ; CURRENT APPLICATION NUMBER: US/09/484,996  
 ; CURRENT FILING DATE: 2000-01-18  
 ; PRIOR APPLICATION NUMBER: 09/276,820  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1998-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-484-996-22

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGTGTGTGGAGGTGCGTGAAGTGTGCGGAGCAAAATTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTTGTGTGTGGAGGTGCGTGAAGTGTGCGGAGCAAAATTAAGCTACA 1211  
 QY 61 ACAAGCAGAGGCTTGACCGCAATTCATGAGAAATCTGCTTAGGGTTAGCGGTTTGGG 120  
 Db 1212 ACAAGCAGAGGCTTGACCGCAATTCATGAGAAATCTGCTTAGGGTTAGCGGTTTGGG 1271  
 QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 1272 CTGCTTCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 1331  
 QY 181 CGAAAAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
 Db 1332 CGCCAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGG 300  
 Db 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGG 1451  
 QY 301 TAAAGTAGGTTAGCAACATGCTTACAGGAGGAGAAACCGTGTGATTCGCGATTGG 360

Db 1452 TAACGATGACTAGCAACATGCCCTTAAGGAGAGAAAACCGCTGCATCCGATTGG 1511  
 QY 361 TGGAGTAAGTGTGATGATGCTGCTTATTAGGAGGCAACAGAGCGGTCTGACATGGA 420  
 Db 1512 TGGAGTAAGTGTGATGATGCTGCTTATTAGGAGGCAACAGAGCGGTCTGACATGGA 1571  
 QY 421 TTGGACGAACCACTAAATTCGGATTGCGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 479  
 Db 1572 TTGGACGAACCACTAAATTCGGATTGCGAGAT-ATTGTAATTAAGTGCCTAGCTCGAT 1631  
 QY 480 ACAATAAGCCCAATTGACCAATTCACCAATTTGGTGTGCACCTC 523  
 Db 1632 ACAATAAGCCCAATTGACCAATTCACCAATTTGGTGTGCACCTC 1675

RESULT 38  
 US-09-484-996-23  
 ; Sequence 23, Application US/09484996  
 ; Patent No. 6623958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003H  
 ; CURRENT APPLICATION NUMBER: US/09/484,996  
 ; CURRENT FILING DATE: 2000-01-18  
 ; PRIOR APPLICATION NUMBER: 09/276,820  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1998-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 23  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-484-996-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGTGTGTGGAGGTGCGTGAAGTGTGCGGAGCAAAATTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTTGTGTGTGGAGGTGCGTGAAGTGTGCGGAGCAAAATTAAGCTACA 1211  
 QY 61 ACAAGCAGAGGCTTGACCGCAATTCATGAGAAATCTGCTTAGGGTTAGCGGTTTGGG 120  
 Db 1212 ACAAGCAGAGGCTTGACCGCAATTCATGAGAAATCTGCTTAGGGTTAGCGGTTTGGG 1271  
 QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 1272 CTGCTTCGCGATGTACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 1331  
 QY 181 CGAAAAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
 Db 1332 CGCCAGCGGGCTTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGG 300  
 Db 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGG 1451  
 QY 301 TAAAGTAGGTTAGCAACATGCTTACAGGAGGAGAAACCGTGTGATTCGCGATTGG 360

QY 241 TTTTGCATAGGAGGGGAAATGCTATGCAATACCTTGTAGTCTTGCAATGG 300  
 Db 1392 TTTTGCATAGGAGGGGAAATGCTATGCAATACCTTGTAGTCTTGCAATGG 1451  
 QY 301 TAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
 Db 1452 TAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1511  
 QY 361 TGGAGTAAAGTGGTACGATGCTTATAGAGGCAACAGACGGGCTGCAATGGA 420  
 Db 1512 TGGAGTAAAGTGGTACGATGCTTATAGAGGCAACAGACGGGCTGCAATGGA 1571  
 QY 421 TTGAGCAACCACTAAATTCGGATTCGATTCGATTCGATTCGATTCGAT 479  
 Db 1572 TTGAGCAACCACTAAATTCGGATTCGATTCGATTCGATTCGATTCGAT 1631  
 QY 480 ACAATAAGCCATTTGACCACTACCACTACCACTACCACTACCACTACCA 523  
 Db 1632 ACAATAAGCCATTTGACCACTACCACTACCACTACCACTACCACTACCA 1675

RESULT 39  
 US-09-484-996-28  
 ; Sequence 28, Application US/09484996  
 ; Patent No. 6623958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERP, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; TITLE OF INVENTION: ENDOGENOUS GENES  
 ; FILE REFERENCE: 0221-0003H  
 ; CURRENT APPLICATION NUMBER: US/09/484,996  
 ; PRIOR FILING DATE: 2000-01-18  
 ; PRIOR APPLICATION NUMBER: 09/276,820  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1998-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 28  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-484-996-28

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGTGTTGGAGTCCGCTGAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTTGTGTTGGAGTCCGCTGAGTGGCGGAGCAAAATTTAAGCTACA 1211  
 QY 61 ACAAGGCAAGCTTGCACCAATTCGATGAGGTTAGCGGTTAGCGGTTTTCG 120  
 Db 1212 ACAAGGCAAGCTTGCACCAATTCGATGAGGTTAGCGGTTAGCGGTTTTCG 1271  
 QY 121 CTGCTCCGATGATGACGGGCAAGATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 180

Db 1272 CTGCTCCGATGATGACGGGCAAGATTCGCGTATCTGAGGGGACTAGGCTGTGTTAGG 1331  
 QY 181 CGAAACCGGGGCTTCCGTTGACGCGGTTAGAGTCCCTCAGGATATAGTGTTCGC 240  
 Db 1332 CGCCACCGGGGCTTCCGTTGACGCGGTTAGAGTCCCTCAGGATATAGTGTTCGC 1391  
 QY 241 TTTTGCATAGGAGGGGAAATGCTATGCAATACCTTGTAGTCTTGCAATGG 300  
 Db 1392 TTTTGCATAGGAGGGGAAATGCTATGCAATACCTTGTAGTCTTGCAATGG 1451  
 QY 301 TAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
 Db 1452 TAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1511  
 QY 361 TGGAGTAAAGTGGTACGATGCTTATAGAGGCAACAGACGGGCTGCAATGGA 420  
 Db 1512 TGGAGTAAAGTGGTACGATGCTTATAGAGGCAACAGACGGGCTGCAATGGA 1571  
 QY 421 TTGAGCAACCACTAAATTCGGATTCGATTCGATTCGATTCGATTCGAT 479  
 Db 1572 TTGAGCAACCACTAAATTCGGATTCGATTCGATTCGATTCGATTCGAT 1631  
 QY 480 ACAATAAGCCATTTGACCACTACCACTACCACTACCACTACCACTACCA 523  
 Db 1632 ACAATAAGCCATTTGACCACTACCACTACCACTACCACTACCACTACCA 1675

RESULT 40  
 US-09-479-123-22  
 ; Sequence 22, Application US/09479123  
 ; Patent No. 6670185  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERP, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; TITLE OF INVENTION: ENDOGENOUS GENES  
 ; FILE REFERENCE: 0221-0003B  
 ; CURRENT APPLICATION NUMBER: US/09/479,123  
 ; PRIOR FILING DATE: 2000-01-07  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-479-123-22

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTTGTGTTGGAGTCCGCTGAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 1152 CTGCTCCCTGCTTGTGTTGGAGTCCGCTGAGTGGCGGAGCAAAATTTAAGCTACA 1211

QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAGAAATCTGTTAGGGTTAGCGCTTTTGG 120  
 Db |||||  
 QY 1212 ACAAGCAAGGCTTGACCGCAATTCATGAGAAATCTGTTAGGGTTAGCGCTTTTGG 1271  
 Db |||||  
 QY 121 CTGCTTCGGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGGTGTGTTTGG 180  
 Db |||||  
 QY 181 CGAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTGTTTGG 240  
 Db |||||  
 QY 1332 CGCCAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTGTTTGG 1391  
 Db |||||  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Db |||||  
 QY 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451  
 Db |||||  
 QY 301 TAAGCATGATGTAGCAATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATGG 360  
 Db |||||  
 QY 1452 TAAGCATGATGTAGCAATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATGG 1511  
 Db |||||  
 QY 361 TGGAGTAAAGTGTGATGATCGTCTTATAGGAGGAGAAAGACCGTGCATGCCGATGG 420  
 Db |||||  
 QY 1512 TGGAGTAAAGTGTGATGATCGTCTTATAGGAGGAGAAAGACCGTGCATGCCGATGG 1571  
 Db |||||  
 QY 421 TTGACGACACCTAAATTCGGCATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 Db |||||  
 QY 1572 TTGACGACACCTAAATTCGGCATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631  
 Db |||||  
 QY 480 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
 Db |||||  
 QY 1632 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 1675  
 Db |||||

RESULT 41  
 US-09-479-123-23  
 ; Sequence 23, Application US/09479123  
 ; Patent No. 6670185  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003B  
 ; CURRENT APPLICATION NUMBER: US/09/479,123  
 ; CURRENT FILING DATE: 2000-01-07  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 23  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; US-09-479-123-23

Query Match 95.8%; Score 500.8; DB 4; Length 9737;  
 Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGCTTGGAGTCTGAGTAGTGGCGAGCAAAATTTTAACTACA 60  
 Db |||||  
 QY 1152 CTGCTCCCTGCTTGTGCTTGGAGTCTGAGTAGTGGCGAGCAAAATTTTAACTACA 1211  
 Db |||||  
 QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAGAAATCTGTTAGGGTTAGCGCTTTTGG 120  
 Db |||||  
 QY 1212 ACAAGCAAGGCTTGACCGCAATTCATGAGAAATCTGTTAGGGTTAGCGCTTTTGG 1271  
 Db |||||  
 QY 121 CTGCTTCGGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGGTGTGTTTGG 180  
 Db |||||  
 QY 1272 CTGCTTCGGCATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGGTGTGTTTGG 1331  
 Db |||||  
 QY 181 CGAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTGTTTGG 240  
 Db |||||  
 QY 1332 CGCCAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTGTGTTTGG 1391  
 Db |||||  
 QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300  
 Db |||||  
 QY 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1451  
 Db |||||  
 QY 301 TAAGCATGATGTAGCAATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATGG 360  
 Db |||||  
 QY 1452 TAAGCATGATGTAGCAATGCTTACAGGAGGAGAAAGACCGTGCATGCCGATGG 1511  
 Db |||||  
 QY 361 TGGAGTAAAGTGTGATGATCGTCTTATAGGAGGAGAAAGACCGTGCATGCCGATGG 420  
 Db |||||  
 QY 1512 TGGAGTAAAGTGTGATGATCGTCTTATAGGAGGAGAAAGACCGTGCATGCCGATGG 1571  
 Db |||||  
 QY 421 TTGACGACACCTAAATTCGGCATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
 Db |||||  
 QY 1572 TTGACGACACCTAAATTCGGCATTCGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 1631  
 Db |||||  
 QY 480 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 523  
 Db |||||  
 QY 1632 ACAATAAGCCATTGACCATTCACCATTTGGTGTGCACCTC 1675  
 Db |||||

RESULT 42  
 US-09-479-123-28  
 ; Sequence 28, Application US/09479123  
 ; Patent No. 6670185  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERF, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003B  
 ; CURRENT APPLICATION NUMBER: US/09/479,123  
 ; CURRENT FILING DATE: 2000-01-07  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 28  
 ; LENGTH: 9737  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8347)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8499)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; US-09-479-123-28



US-09-479-123-28

```

Query Match          95.8%; Score 500.8; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1152 CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1211
QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAGAAATCTGCTTAGGGTTAGCGTTTGGG 120
DB 1212 ACAAGGCAAGGCTTGACCGACAAATTCATGAGAAATCTGCTTAGGGTTAGCGTTTGGG 1271
QY 121 CTGCTTCCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 180
DB 1272 CTGCTTCCGCGATGTACGGGCGAGATATACGCGTATCTGAGGGGACTAGGGTGTGTTAGG 1331
QY 181 CGAAAGCGGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGGATATAGTATTTGGC 240
DB 1332 CGCCAGCGGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGGATATAGTATTTGGC 1391
QY 241 TTTTGCATAGAGGAGGGGAAATGTAGTCTTATGCAATATCTCTGTAGTCTTGTGCAACATGG 300
DB 1392 TTTTGCATAGAGGAGGGGAAATGTAGTCTTATGCAATATCTCTGTAGTCTTGTGCAACATGG 1451
QY 301 TAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAGCACCGTGCAATGCCGATTGG 360
DB 1452 TAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAGCACCGTGCAATGCCGATTGG 1511
QY 361 TGGAGTAAAGTGTAGCATCTGTCCTTATGAGAGGCAACAGACGGGTTCTGACATGGA 420
DB 1512 TGGAGTAAAGTGTAGCATCTGTCCTTATGAGAGGCAACAGACGGGTTCTGACATGGA 1571
QY 421 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTAATTAAGTGTAGTCTGAT 479
DB 1572 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTAATTAAGTGTAGTCTGAT 1631
QY 480 ACAATAAGCGCAATTCACCAATTCACCAATTCACCAATTCGATGTGCACTC 523
DB 1632 ACAATAAGCGCAATTCACCAATTCACCAATTCACCAATTCGATGTGCACTC 1675

```

RESULT 43

```

US-09-479-122-24
; Sequence 24, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

```

; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-24

Query Match          95.8%; Score 500.8; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1286 CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1345
QY 61 ACAAGGCAAGGCTTGACCGCAAAATTCATGAGAAATCTGCTTAGGGTTAGCGTTTGGG 120
DB 1346 ACAAGGCAAGGCTTGACCGCAAAATTCATGAGAAATCTGCTTAGGGTTAGCGTTTGGG 1405
QY 121 CTGCTTCCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 180
DB 1406 CTGCTTCCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 1465
QY 181 CGAAAGCGGGGCTTCGGTTGTAAGCGGTTAGAGTCCCTCAGGATATAGTATTTGGC 240
DB 1466 CGCCAGCGGGGCTTCGGTTGTAAGCGGTTAGAGTCCCTCAGGATATAGTATTTGGC 1525
QY 241 TTTTGCATAGAGGAGGGGAAATGTAGTCTTATGCAATATCTCTGTAGTCTTGTGCAACATGG 300
DB 1526 TTTTGCATAGAGGAGGGGAAATGTAGTCTTATGCAATATCTCTGTAGTCTTGTGCAACATGG 1585
QY 301 TAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAGCACCGTGCAATGCCGATTGG 360
DB 1586 TAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAGCACCGTGCAATGCCGATTGG 1645
QY 361 TGGAGTAAAGTGTAGCATCTGTCCTTATGAGAGGCAACAGACGGGTTCTGACATGGA 420
DB 1646 TGGAGTAAAGTGTAGCATCTGTCCTTATGAGAGGCAACAGACGGGTTCTGACATGGA 1705
QY 421 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTAATTAAGTGTAGTCTGAT 479
DB 1706 TTGACGACCACTAAATTCGCAATTCGAGAGAT-ATTGTAATTAAGTGTAGTCTGAT 1765
QY 480 ACAATAAGCGCAATTCACCAATTCACCAATTCACCAATTCGATGTGCACTC 523
DB 1766 ACAATAAGCGCAATTCACCAATTCACCAATTCACCAATTCGATGTGCACTC 1809

```

RESULT 44

```

US-09-484-997-24
; Sequence 24, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33

```

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-24

Query Match          95.8%; Score 500.8; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 7,1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db 1286 CTGCTCCCTGCTGTGTGTTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 1345
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAACTCTGTTAGGTTAGCGCTTTTGG 120
Db 1346 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAACTCTGTTAGGTTAGCGCTTTTGG 1405
QY 121 CTCCTTCGCGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180
Db 1406 CTCCTTCGCGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 1465
QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGATATAGTATTTGCG 240
Db 1466 CGCCACGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGATATAGTATTTGCG 1525
QY 241 TTTTGCATAGGAGGGGAAATGTAAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 300
Db 1526 TTTTGCATAGGAGGGGAAATGTAAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 1585
QY 301 TAACGATAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGCCGATTGG 360
Db 1586 TAACGATAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGCCGATTGG 1645
QY 361 TGGAGTAGGTGGTGCATCGTCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420
Db 1646 TGGAGTAGGTGGTGCATCGTCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1705
QY 421 TTGGACGAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTAGTGCCTAGCTCGAT 479
Db 1706 TTGGACGAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTAGTGCCTAGCTCGAT 1765
QY 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGTTGTCACCTC 523
Db 1766 ACAATAAGCCATTGACCAATTCACCAATTCGATGTTGTCACCTC 1809

RESULT 45
US-09-481-355-24
; Sequence 25, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: SHERE, BRUCE
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223

```

```

; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-24

Query Match          95.8%; Score 500.8; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 7,1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGTTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db 1286 CTGCTCCCTGCTGTGTGTTGGAGGTGCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 1345
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAACTCTGTTAGGTTAGCGCTTTTGG 120
Db 1346 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAACTCTGTTAGGTTAGCGCTTTTGG 1405
QY 121 CTCCTTCGCGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 180
Db 1406 CTCCTTCGCGATGTACGGGCCAGATATTCGGTATCTGAGGGGACTAGGGTGTGTTAGG 1465
QY 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGATATAGTATTTGCG 240
Db 1466 CGCCACGCGGGCTTCGGTTGTACGGGTTAGGATCCCTCAGATATAGTATTTGCG 1525
QY 241 TTTTGCATAGGAGGGGAAATGTAAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 300
Db 1526 TTTTGCATAGGAGGGGAAATGTAAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGG 1585
QY 301 TAACGATAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGCCGATTGG 360
Db 1586 TAACGATAGTTAGCAACATGCTTACAGGAGAGAAAAGCAACCGTGCAATGCCGATTGG 1645
QY 361 TGGAGTAGGTGGTGCATCGTCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420
Db 1646 TGGAGTAGGTGGTGCATCGTCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1705
QY 421 TTGGACGAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTAGTGCCTAGCTCGAT 479
Db 1706 TTGGACGAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTAGTGCCTAGCTCGAT 1765
QY 480 ACAATAAGCCATTGACCAATTCACCAATTCGATGTTGTCACCTC 523
Db 1766 ACAATAAGCCATTGACCAATTCACCAATTCGATGTTGTCACCTC 1809

RESULT 46
US-09-481-282-24
; Sequence 24, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERE, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282

```

```

; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-24

Query Match      95.8%; Score 500.8; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1286 CTGCTCCCTGCTTGTGGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1345
QY 61 ACAAGCAAGCTTTGACCCGCAATTCATGAAGAATCTCTTAGGGTAGGGTTTGGC 120
DB 1346 ACAAGCAAGCTTTGACCCGCAATTCATGAAGAATCTCTTAGGGTAGGGTTTGGC 1405
QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 180
DB 1406 CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 1465
QY 181 CGAAAGCGGGCTTGGTGTGACGGGCTTACGGGTTAGGAGTCCCTCAGGATATAGTTCGC 240
DB 1526 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCAACATGG 1585
QY 301 TAACGATGAGTTAGCAACATGTCCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGG 360
DB 1586 TAACGATGAGTTAGCAACATGTCCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGG 1645
QY 361 TGGAGTAAAGTGTGATGATGCTGCTTATAGAGGCAACAGACGGGCTGACATGGA 420
DB 1646 TGGAGTAAAGTGTGATGATGCTGCTTATAGAGGCAACAGACGGGCTGACATGGA 1705
QY 421 TTGGACGAACCACTAAATTCGCAATTCACCAATTTGGTGTGCACTC 479
DB 1706 TTGGACGAACCACTAAATTCGCAATTCACCAATTTGGTGTGCACTC 1765
QY 480 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACTC 523
DB 1766 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACTC 1809

```

```

RESULT 47
US-09-455-659A-24
; Sequence 24, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE

```

```

; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-24

Query Match      95.8%; Score 500.8; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 7.1e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTTGTGGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
DB 1286 CTGCTCCCTGCTTGTGGTGGAGGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 1345
QY 61 ACAAGCAAGCTTTGACCCGCAATTCATGAAGAATCTCTTAGGGTAGGGTTTGGC 120
DB 1346 ACAAGCAAGCTTTGACCCGCAATTCATGAAGAATCTCTTAGGGTAGGGTTTGGC 1405
QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 180
DB 1406 CTGCTTCGCGATGTACGGGCGAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGG 1465
QY 181 CGAAAGCGGGCTTGGTGTGACGGGCTTACGGGTTAGGAGTCCCTCAGGATATAGTTCGC 240
DB 1466 CGCCACAGCGGGCTTGGTGTGACGGGTTAGGAGTCCCTCAGGATATAGTTCGC 1525
QY 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCAACATGG 300
DB 1526 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCAACATGG 1585
QY 301 TAACGATGAGTTAGCAACATGTCCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGG 360
DB 1586 TAACGATGAGTTAGCAACATGTCCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGG 1645
QY 361 TGGAGTAAAGTGTGATGATGCTGCTTATAGAGGCAACAGACGGGCTGACATGGA 420
DB 1646 TGGAGTAAAGTGTGATGATGCTGCTTATAGAGGCAACAGACGGGCTGACATGGA 1705
QY 421 TTGGACGAACCACTAAATTCGCAATTCACCAATTTGGTGTGCACTC 479
DB 1706 TTGGACGAACCACTAAATTCGCAATTCACCAATTTGGTGTGCACTC 1765
QY 480 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACTC 523
DB 1766 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACTC 1809

```

RESULT 48  
US-09-484-996-24  
; Sequence 24, Application US/09484996  
; Patent No. 6623958  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERP, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; FILE REFERENCE: 0221-0003H  
; CURRENT APPLICATION NUMBER: US/09/484,996  
; CURRENT FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1998-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 9871  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8481)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; NAME/KEY: modified\_base  
; LOCATION: (8633)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-484-996-24

Query Match 95.8%; Score 500.8; DB 4; Length 9871;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60  
DB 1286 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 1345  
QY 61 ACAAGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGCTTAGCGCTTTTGGC 120  
DB 1346 ACAAGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGCTTAGCGCTTTTGGC 1405  
QY 121 CTGCTTCGGATGATACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
DB 1406 CTGCTTCGGATGATACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 1465  
QY 181 CGAAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTACTTTCCG 240  
DB 1466 CGCCACGGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTACTTTCCG 1525  
QY 241 TTTTGCATAGGAGGGGAAATGACTTATGCAATACCTCTTAGTCTTTGCAACATGG 300  
DB 1526 TTTTGCATAGGAGGGGAAATGACTTATGCAATACCTCTTAGTCTTTGCAACATGG 1585  
QY 301 TAACGATGATGATACCGCTTACAGGAGAGAAAGACCGTGCATGCGGATTGG 360  
DB 1586 TAACGATGATGATACCGCTTACAGGAGAGAAAGACCGTGCATGCGGATTGG 1645  
QY 361 TGGAGTAAGGTGATGATGCGCTTATAGAGGCAACAGACGGGCTGACATGA 420  
DB 1646 TGGAGTAAGGTGATGATGCGCTTATAGAGGCAACAGACGGGCTGACATGA 1705  
QY 421 TTGAGCAACCACTAAATTCGCATATGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGAT 479  
DB 1706 TTGAGCAACCACTAAATTCGCATATGCAGAGATATTGTATTAAAGTGCCTAGCTCGAT 1765

QY 480 ACAATAAAGCCATTGTGACATTACCAACATTTGGTGTGCACCTC 523  
DB 1766 ACAATAAAGCCATTGTGACATTACCAACATTTGGTGTGCACCTC 1809

RESULT 49  
US-09-479-123-24  
; Sequence 24, Application US/09479123  
; Patent No. 6670185  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERP, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; FILE REFERENCE: 0221-0003B  
; CURRENT APPLICATION NUMBER: US/09/479,123  
; CURRENT FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 9871  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8481)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; NAME/KEY: modified\_base  
; LOCATION: (8633)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-479-123-24

Query Match 95.8%; Score 500.8; DB 4; Length 9871;  
Best Local Similarity 98.5%; Pred. No. 7.1e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 60  
DB 1286 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTAAGCTACA 1345  
QY 61 ACAAGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGCTTAGCGCTTTTGGC 120  
DB 1346 ACAAGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGCTTAGCGCTTTTGGC 1405  
QY 121 CTGCTTCGGATGATACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
DB 1406 CTGCTTCGGATGATACGGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 1465  
QY 181 CGAAAAGCGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTACTTTCCG 240  
DB 1466 CGCCACGGGGCTTCGGTGTACGGGTTAGGAGTCCCTCAGGATATAGTACTTTCCG 1525  
QY 241 TTTTGCATAGGAGGGGAAATGACTTATGCAATACCTCTTAGTCTTTGCAACATGG 300  
DB 1526 TTTTGCATAGGAGGGGAAATGACTTATGCAATACCTCTTAGTCTTTGCAACATGG 1585  
QY 301 TAACGATGATGATACCGCTTACAGGAGAGAAAGACCGTGCATGCGGATTGG 360  
DB 1586 TAACGATGATGATACCGCTTACAGGAGAGAAAGACCGTGCATGCGGATTGG 1645  
QY 361 TGGAGTAAGGTGATGATGCGCTTATAGAGGCAACAGACGGGCTGACATGA 420

Db 1646 TGAAGTAAGTGGTACGATCGTCCCTATTAGGAAGCAACAGACAGGTCTGCATGGA 1705  
 Qy 421 TTGACGAAACCACTAAATTCGCATTCAGAGAT-ATTGTAATTAAAGTCCCTAGCTCGAT 479  
 Db 1706 TTGACGAAACCACTAAATTCGCATTCAGAGAT-ATTGTAATTAAAGTCCCTAGCTCGAT 1765  
 Qy 480 ACAATAAACCCATTGACCAATTCACCAATTTGGTGGACCTC 523  
 Db 1766 ACAATAAACCCATTGACCAATTCACCAATTTGGTGGACCTC 1809

RESULT 50  
 US-09-479-122-25  
 ; Sequence 25, Application US/09479122  
 ; Patent No. 6410266  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERP, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003C  
 ; CURRENT APPLICATION NUMBER: US/09/479,122  
 ; PRIOR FILING DATE: 2000-03-07  
 ; PRIOR APPLICATION NUMBER: 09/276,820  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 25  
 ; LENGTH: 10060  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8670)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8822)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-479-122-25

Query Match 95.8%; Score 500.8; DB 4; Length 10060;  
 Best Local Similarity 98.5%; Pred. No. 7.2e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 Qy 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
 Db 1475 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 1534  
 Qy 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGGG 120  
 Db 1535 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGGG 1594  
 Qy 121 CTGCTTCGCGATGTACGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTCTTAGG 180  
 Db 1595 CTGCTTCGCGATGTACGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTCTTAGG 1654  
 Qy 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATATGATGTTTGGC 240  
 Db 1655 CGCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATATGATGTTTGGC 1714  
 Qy 241 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTAGTCTTTCGCAACATGG 300  
 Db 1715 TTTTGCATAGGAGGGGAAATAGTCTTATGCAATCTCTTAGTCTTTCGCAACATGG 1774

Qy 301 TAAAGTGGTGGTACCAATCGCTTACAGAGAGAGAAAAAGCCGTCATGCCATTGG 360  
 Db 1775 TAAAGTGGTGGTACCAATCGCTTACAGAGAGAGAAAAAGCCGTCATGCCATTGG 1834  
 Qy 361 TGAAGTAAGTGGTACGATCGTCCCTATTAGGAAGCAACAGACAGGTCTGCATGGA 420  
 Db 1835 TGAAGTAAGTGGTACGATCGTCCCTATTAGGAAGCAACAGACAGGTCTGCATGGA 1894  
 Qy 421 TTGACGAAACCACTAAATTCGCATTCAGAGAT-ATTGTAATTAAAGTCCCTAGCTCGAT 479  
 Db 1895 TTGACGAAACCACTAAATTCGCATTCAGAGAT-ATTGTAATTAAAGTCCCTAGCTCGAT 1954  
 Qy 480 ACAATAAACCCATTGACCAATTCACCAATTTGGTGGACCTC 523  
 Db 1955 ACAATAAACCCATTGACCAATTCACCAATTTGGTGGACCTC 1998

RESULT 51  
 US-09-484-997-25  
 ; Sequence 25, Application US/09484997  
 ; Patent No. 6524818  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HARRINGTON, JOHN J.  
 ; APPLICANT: SHERP, BRUCE  
 ; APPLICANT: RUNDLETT, STEPHEN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
 ; FILE REFERENCE: 0221-0003J  
 ; CURRENT APPLICATION NUMBER: US/09/484,997  
 ; PRIOR FILING DATE: 2000-01-18  
 ; PRIOR APPLICATION NUMBER: 09/276,820  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 09/159,643  
 ; PRIOR FILING DATE: 1998-09-24  
 ; PRIOR APPLICATION NUMBER: 08/941,223  
 ; PRIOR FILING DATE: 1997-09-26  
 ; PRIOR APPLICATION NUMBER: 09/263,814  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 09/253,022  
 ; PRIOR FILING DATE: 1999-02-19  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn ver. 2.1  
 ; SEQ ID NO 25  
 ; LENGTH: 10060  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8670)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (8822)  
 ; OTHER INFORMATION: a, c, t, g, other or unknown  
 US-09-484-997-25

Query Match 95.8%; Score 500.8; DB 4; Length 10060;  
 Best Local Similarity 98.5%; Pred. No. 7.2e-169;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 Qy 1 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 60  
 Db 1475 CTGCTCCCTGCTGTGTGGAGTTCGCTGAGTAGTGCAGCAAAATTTAAGCTACA 1534  
 Qy 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGGG 120  
 Db 1535 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTGCTTAGGGTTAGCGGTTTGGG 1594  
 Qy 121 CTGCTTCGCGATGTACGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTCTTAGG 180  
 Db 1595 CTGCTTCGCGATGTACGGCCAGATATTCGGGTATCTGAGGGGACTAGGGTGTCTTAGG 1654  
 Qy 181 CGAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATATGATGTTTGGC 240

Db 1655 CGCCACGCGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGGATATAGTAGTTGCG 1714

Qy 241 TTTTGGCATAGGAGGGGGAATAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGG 300

Db 1715 TTTTGGCATAGGAGGGGGAATAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGG 1774

Qy 301 TAACGATGAGTTAGCAACATGCTCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360

Db 1775 TAACGATGAGTTAGCAACATGCTCTTACAAGGAGAGAAAGCAACCGTGCATGCCGATTGG 1834

Qy 361 TGGAGTAAGTGGTACGATCGTCTTATAGGAGGACACAGAGGCTTGCATGGA 420

Db 1835 TGGAGTAAGTGGTACGATCGTCTTATAGGAGGACACAGAGGCTTGCATGGA 1894

Qy 421 TTGACGAACCACTAAATTCGCAATTCGAGAT - ATTGTATTTAAGTGGTGCACCTC 479

Db 1895 TTGACGAACCACTAAATTCGCAATTCGAGAT - ATTGTATTTAAGTGGTGCACCTC 1954

Qy 480 ACAATAAGCCCATTTGACCAATTCACCAATTTGGTGGTGCACCTC 523

Db 1955 ACAATAAGCCCATTTGACCAATTCACCAATTTGGTGGTGCACCTC 1998

RESULT 52

US-09-481-355-25

; Sequence 25, Application US/09481355

; Patent No. 6524824

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERP BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE OF INVENTION: ENDGENOUS GENES

; FILE REFERENCE: 0221-0003F

; CURRENT APPLICATION NUMBER: US/09/481,355

; CURRENT FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 10060

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8670)

; OTHER INFORMATION: a, c, t, g, other or unknown

; NAME/KEY: modified\_base

; LOCATION: (8822)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-09-481-355-25

Query Match 95.8%; Score 500.8; DB 4; Length 10060;

Best Local Similarity 98.5%; Pred. No. 7.2e-169;

Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTCTGTTGTTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60

Db 1475 CTGCTCCCTCTGTTGTTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 1534

Qy 61 ACAAGGCAAGGCTTACCGCAATTCGATCAAGAAATCTGCTTAGGCTTAGGCGTTTTCG 120

Db 1535 ACAAGGCAAGGCTTACCGCAATTCGATCAAGAAATCTGCTTAGGCTTAGGCGTTTTCG 1594

Qy 121 CTGCTTCGATGATGAGGCGCAGATATTCGCTATCTGAGGGACTAGGCTGTGTTAGG 180

Db 1595 CTGCTTCGATGATGAGGCGCAGATATTCGCTATCTGAGGGACTAGGCTGTGTTAGG 1654

Qy 181 CGAAAAACGCGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 240

Db 1655 CGCCACGCGGGCTTCGGTTGACGGGTTAGAGTCCCTCAGGATATAGTAGTTTCGC 1714

Qy 241 TTTTGCATAGGAGGGGGAATGATGATCTTATGCAATACCTTTGTAGTCTTGCACATGG 300

Db 1715 TTTTGCATAGGAGGGGGAATGATGATCTTATGCAATACCTTTGTAGTCTTGCACATGG 1774

Qy 301 TAAAGTATGATAGCAACATCCCTTCAAGGAGAGAAAGCAACCGTGCATGCCGATTGG 360

Db 1775 TAAAGTATGATAGCAACATCCCTTCAAGGAGAGAAAGCAACCGTGCATGCCGATTGG 1834

Qy 361 TGGAGTAAGTGGTACGATCGTCTTATAGGAGGACACAGAGGCTTGCATGGA 420

Db 1835 TGGAGTAAGTGGTACGATCGTCTTATAGGAGGACACAGAGGCTTGCATGGA 1894

Qy 421 TTGACGAACCACTAAATTCGCAATTCGAGAT - ATTGTATTTAAGTGGTGCACCTC 479

Db 1895 TTGACGAACCACTAAATTCGCAATTCGAGAT - ATTGTATTTAAGTGGTGCACCTC 1954

Qy 480 ACAATAAGCCCATTTGACCAATTCACCAATTTGGTGGTGCACCTC 523

Db 1955 ACAATAAGCCCATTTGACCAATTCACCAATTTGGTGGTGCACCTC 1998

RESULT 53

US-09-481-282-25

; Sequence 25, Application US/09481282

; Patent No. 6541221

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERP BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE OF INVENTION: ENDGENOUS GENES

; FILE REFERENCE: 0221-0003US

; CURRENT APPLICATION NUMBER: US/09/481,282

; CURRENT FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 10060

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8670)

; OTHER INFORMATION: a, c, t, g, other or unknown

; NAME/KEY: modified\_base

; LOCATION: (8822)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-09-481-282-25

Query Match 95.8%; Score 500.8; DB 4; Length 10060;

Best Local Similarity 98.5%; Pred. No. 7.2e-169;

Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 CTGCTCCCTCTGTTGTTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60

Db 1475 CTGCTCCCTCTGTTGTTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 1534

```

QY 61 ACAGGCAAGGCTTACCGCAATTCGATGAGAACTCTAGGTTAGCGTTTGG 120
|
|
|
Db 1535 ACAGGCAAGGCTTACCGCAATTCGATGAGAACTCTAGGTTAGCGTTTGG 1594
|
|
|
QY 121 CTGCTTCGCGATGACGGGCGAGATATTCGCTATCTGAGGGAATAGGTTAGG 180
|
|
|
Db 1595 CTGCTTCGCGATGACGGGCGAGATATTCGCTATCTGAGGGAATAGGTTAGG 1654
|
|
|
QY 181 CGAAAAAGCGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTTCGC 240
|
|
|
Db 1555 CGCCAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTTCGC 1714
|
|
|
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
|
|
|
Db 1715 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1774
|
|
|
QY 301 TAACGATGATGATGACATGCTTACAGGAGGAAAGCAACCGTGCATGCCGATTGG 360
|
|
|
Db 1775 TAACGATGATGATGACATGCTTACAGGAGGAAAGCAACCGTGCATGCCGATTGG 1834
|
|
|
QY 361 TGGAGTAAAGTGTGATGATGCTTACAGGAGGAAAGCAACCGTGCATGCCGATTGG 420
|
|
|
Db 1835 TGGAGTAAAGTGTGATGATGCTTACAGGAGGAAAGCAACCGTGCATGCCGATTGG 1894
|
|
|
QY 421 TTGGACGAACCACTAAATTCGGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479
|
|
|
Db 1895 TTGGACGAACCACTAAATTCGGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1954
|
|
|
QY 480 ACAATAAGCGCATTTGACCATTCACCATTCGATGTCGACCTC 523
|
|
|
Db 1955 ACAATAAGCGCATTTGACCATTCACCATTCGATGTCGACCTC 1998
|
|
|

```

RESULT 54

```

US-09-455-659A-25
/ Sequence 25, Application US/09455659A
/ Patent No. 6602686
/ GENERAL INFORMATION:
/ APPLICANT: HARRINGTON, JOHN J.
/ APPLICANT: SHERF, BRUCE
/ APPLICANT: RUNDLETT, STEPHEN
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
/ FILE REFERENCE: 0221-0003A
/ CURRENT APPLICATION NUMBER: US/09/455,659A
/ CURRENT FILING DATE: 1999-12-07
/ PRIOR APPLICATION NUMBER: 09/276,820
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 09/263,814
/ PRIOR FILING DATE: 1999-03-08
/ PRIOR APPLICATION NUMBER: 09/253,022
/ PRIOR FILING DATE: 1999-02-19
/ PRIOR APPLICATION NUMBER: 09/159,643
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 08/941,223
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 10060
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (8670)
/ OTHER INFORMATION: a, c, t, g, other or unknown
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (8822)
/ OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-25

```

```

Query Match 95.8%; Score 500.8; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 7.2e-169;
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 1 CTGCTTCGCTTGTGTGTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTAAGCTTACA 60
|
|
|
Db 1475 CTGCTTCGCTTGTGTGTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTAAGCTTACA 1534
|
|
|
QY 61 ACAGGCAAGGCTTACCGCAATTCGATGAGAACTCTAGGTTAGCGTTTGG 120
|
|
|
Db 1535 ACAGGCAAGGCTTACCGCAATTCGATGAGAACTCTAGGTTAGCGTTTGG 1594
|
|
|
QY 121 CTGCTTCGCGATGACGGGCGAGATATTCGCTATCTGAGGGAATAGGTTAGG 180
|
|
|
Db 1555 CGCCAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTTCGC 1654
|
|
|
QY 181 CGAAAAAGCGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTTCGC 240
|
|
|
Db 1655 CGCCAGCGGGCTTCGGTTGTACGGGTAGGAGTCCCTCAGGATATAGTTCGC 1714
|
|
|
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300
|
|
|
Db 1715 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 1774
|
|
|
QY 301 TAACGATGATGATGACATGCTTACAGGAGGAAAGCAACCGTGCATGCCGATTGG 360
|
|
|
Db 1775 TAACGATGATGATGACATGCTTACAGGAGGAAAGCAACCGTGCATGCCGATTGG 1834
|
|
|
QY 361 TGGAGTAAAGTGTGATGATGCTTACAGGAGGAAAGCAACCGTGCATGCCGATTGG 420
|
|
|
Db 1835 TGGAGTAAAGTGTGATGATGCTTACAGGAGGAAAGCAACCGTGCATGCCGATTGG 1894
|
|
|
QY 421 TTGGACGAACCACTAAATTCGGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 479
|
|
|
Db 1895 TTGGACGAACCACTAAATTCGGCATTCGAGAGAT-ATTGTATTTAAGTGCCTAGCTCGAT 1954
|
|
|
QY 480 ACAATAAGCGCATTTGACCATTCACCATTCGATGTCGACCTC 523
|
|
|
Db 1955 ACAATAAGCGCATTTGACCATTCACCATTCGATGTCGACCTC 1998
|
|
|

```

RESULT 55

```

US-09-484-996-25
/ Sequence 25, Application US/09484996
/ Patent No. 6623958
/ GENERAL INFORMATION:
/ APPLICANT: HARRINGTON, JOHN J.
/ APPLICANT: SHERF, BRUCE
/ APPLICANT: RUNDLETT, STEPHEN
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
/ FILE REFERENCE: 0221-0003H
/ CURRENT APPLICATION NUMBER: US/09/484,996
/ CURRENT FILING DATE: 2000-01-18
/ PRIOR APPLICATION NUMBER: 09/276,820
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 09/263,814
/ PRIOR FILING DATE: 1998-03-08
/ PRIOR APPLICATION NUMBER: 09/253,022
/ PRIOR FILING DATE: 1999-02-19
/ PRIOR APPLICATION NUMBER: 09/159,643
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 08/941,223
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 10060
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (8670)
US-09-484-996-25

```

; OTHER INFORMATION: a, c, t, g, other or unknown  
; NAME/KEY: modified\_base  
; LOCATION: (8822)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-484-996-25

Query Match 95.8%; Score 500.8; DB 4; Length 10060;  
Best Local Similarity 98.5%; Pred. No. 7.2e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60  
Db 1475 CTGCTCCCTGCTTGTGTGGAGGTGCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 1534  
  
QY 61 ACAAGCAAGGCTTGACCGCAATTTGCATGAAGATCTGCTTAGGGTGTGGGTTTGG 120  
Db 1535 ACAAGCAAGGCTTGACCGCAATTTGCATGAAGATCTGCTTAGGGTGTGGGTTTGG 1594  
  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTTCGGGTATCTGAGGGGACTAGGGTGTGGT 180  
Db 1595 CTGCTTCGCGATGTACGGGCCAGATATTTCGGGTATCTGAGGGGACTAGGGTGTGGT 1654  
  
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGG 240  
Db 1655 CGCCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGG 1714  
  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Db 1715 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1774  
  
QY 301 TAACGATGAGTTAGCAATGCGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360  
Db 1775 TAACGATGAGTTAGCAATGCGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 1834  
  
QY 361 TGAAGTAGAGTGTGAGTCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420  
Db 1835 TGAAGTAGAGTGTGAGTCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1894  
  
QY 421 TTGGACGAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTAAAGTGCTAGCTCGAT 479  
Db 1955 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 1998

RESULT 56  
US-09-479-123-25  
; Sequence 25, Application US/09479123  
; Patent No. 6670185  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003B  
; CURRENT APPLICATION NUMBER: US/09/479,123  
; CURRENT FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 10060  
; TYPE: DNA

; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8670)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8822)  
; OTHER INFORMATION: a, c, t, g, other or unknown  
US-09-479-123-25  
  
Query Match 95.8%; Score 500.8; DB 4; Length 10060;  
Best Local Similarity 98.5%; Pred. No. 7.2e-169;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60  
Db 1475 CTGCTCCCTGCTTGTGTGGAGGTGCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 1534  
  
QY 61 ACAAGCAAGGCTTGACCGCAATTTGCATGAAGATCTGCTTAGGGTGTGGGTTTGG 120  
Db 1535 ACAAGCAAGGCTTGACCGCAATTTGCATGAAGATCTGCTTAGGGTGTGGGTTTGG 1594  
  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTTCGGGTATCTGAGGGGACTAGGGTGTGGT 180  
Db 1595 CTGCTTCGCGATGTACGGGCCAGATATTTCGGGTATCTGAGGGGACTAGGGTGTGGT 1654  
  
QY 181 CGAAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGG 240  
Db 1655 CGCCCAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTGG 1714  
  
QY 241 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 300  
Db 1715 TTTTGCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTGTAGTCTTGCAACATGG 1774  
  
QY 301 TAACGATGAGTTAGCAATGCGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 360  
Db 1775 TAACGATGAGTTAGCAATGCGCTTACAGGAGGAGAAAGCACCGTGCATGCCGATTGG 1834  
  
QY 361 TGAAGTAGAGTGTGAGTCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 420  
Db 1835 TGAAGTAGAGTGTGAGTCGCTTATTAGGAGGCAACAGACGGGTCTGACATGA 1894  
  
QY 421 TTGGACGAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTAAAGTGCTAGCTCGAT 479  
Db 1895 TTGGACGAACCACTAAATTCGGCATTTGCAGAGAT-ATTGTATTAAAGTGCTAGCTCGAT 1954  
  
QY 480 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 523  
Db 1955 ACAATAAGCGCAATTTGACCAATTCACCAATTTGGTGTGCACCTC 1998

RESULT 57  
US-09-167-322-13  
; Sequence 13, Application US/09167322  
; Patent No. 6365151  
; GENERAL INFORMATION:  
; APPLICANT: Allegheny University of the Health  
; Sciences, Halpern, Michael S.  
; England, James M.  
; TITLE OF INVENTION: CANCER VACCINE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.  
; STREET: Suite 1800, Two Penn Center Plaza  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS



```

/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/167,322
/ FILING DATE: 07-Oct-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US97/00582
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monaco, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 7933-33 PC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 565 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-167-322-13

Query Match      90.2%; Score 472; DB 4; Length 565;
Best Local Similarity 98.0%; Pred. No. 3.1e-159;
Matches 490; Conservative 0; Mismatches 5; Indels 5; Gaps 1;

QY 28 GCTGAGTATGTCGGAGCAAAATTTAAGCTACAAAGCAAGGCTTGACGCAATATGC 87
Db 1 GCTGAGTATGTCGGAGCAAAATTTAAGCTACAAAGCAAGGCTTGACGCAATATGC 60

QY 88 ATGAGAAATCTGTTAGGCTTAGGCTTTGCGCTCTTCGCGATGTACGGGCGAGATAT 147
Db 61 ATGAGAAATCTGTTAGGCTTAGGCTTTGCGCTCTTCGCGATGTACGGGCGAGATAT 120

QY 148 TCGCGTATCTAGGGGACTAGGCTGTGTTAGCGGAAAGCGGGCTTCGGTTGACGCG 207
Db 121 AGCGGTATCTAGGGGACTAGGCTGTGTTAGCGGAAAGCGGGCTTCGGTTGACGCG 180

QY 208 GTTAGAGTCCCTCAGGATATAGTATGCTTTCGCTTTCATAGGAGGCGGAAATGTAGT 267
Db 181 GTTAGAGTCCCTCAGGATATAGTATGCTTTCGCTTTCATAGGAGGCGGAAATGTAGT 240

QY 268 CTTATGCAATATCTTGTAGTCTTGCAACATG-----GTAAGCATGTAGTTAGCAATCG 322
Db 241 CTTATGCAATATCTTGTAGTCTTGCAACATGCTTATGTACATGATGATTAGCAATCG 300

QY 323 CTTACAGAGAGAGAAAGCAGCGGTGATGCGGATTTGTTGGAAGTGAAGTGAATCG 382
Db 301 CTTACAGAGAGAGAAAGCAGCGGTGATGCGGATTTGTTGGAAGTGAAGTGAATCG 360

QY 383 TGCCTTATTAGGAGGCAACAGACGGGCTCTGACATGATGAGCAACCACTAAATTCGG 442
Db 361 TGCCTTATTAGGAGGCAACAGACGGGCTCTGACATGATGAGCAACCACTAAATTCGG 420

QY 443 CATTCGAGATATGTTATTAAGTCTGCTAGCTCGATACAATAACCCCATTTGACCAAT 502
Db 421 CATTCGAGATATGTTATTAAGTCTGCTAGCTCGATACAATAACCCCATTTGACCAAT 480

QY 503 CACCACATTTGTTGCACT 522
Db 481 CACCACATTTGTTGCACT 500

RESULT 58
US-09-470-881-1
; Sequence 1, Application US/09470881
; Patent No. 6685938
; GENERAL INFORMATION:
; APPLICANT: CHERESH, David A.
; APPLICANT: ELICEIRI, Brian
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
/ TITLE OF INVENTION: ANGIOGENESIS AND VASCULAR PERMEABILITY USING SRC OR
/ TITLE OF INVENTION: YES TYROSINE KINASES
/ FILE REFERENCE: TSEI 551.2
/ CURRENT APPLICATION NUMBER: US/09/470,881
/ CURRENT FILING DATE: 1999-12-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11780
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/087,220
/ PRIOR FILING DATE: 1998-05-29
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 11627
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: RCASBP(A) based
/ OTHER INFORMATION: on avian sarcoma virus
/ NAME/KEY: misc feature
/ LOCATION: (7649)..(11258)
/ OTHER INFORMATION: pBR322 sequences
/ NAME/KEY: LTR
/ LOCATION: (7166)..(7494)
/ OTHER INFORMATION: upstream
/ NAME/KEY: LTR
/ LOCATION: (1)..(101)
/ OTHER INFORMATION: upstream (numbering begins at the upstream R)
/ NAME/KEY: misc feature
/ LOCATION: (11394)..(11623)
/ OTHER INFORMATION: U3
/ NAME/KEY: misc feature
/ LOCATION: (1)..(21)
/ OTHER INFORMATION: R
/ NAME/KEY: misc feature
/ LOCATION: (22)..(101)
/ OTHER INFORMATION: U5
/ NAME/KEY: misc feature
/ LOCATION: (102)..(119)
/ NAME/KEY: LTR
/ LOCATION: (7166)..(7494)
/ OTHER INFORMATION: downstream
/ NAME/KEY: misc feature
/ LOCATION: (7166)..(7393)
/ OTHER INFORMATION: U3
/ NAME/KEY: misc feature
/ LOCATION: (7394)..(7414)
/ OTHER INFORMATION: R
/ NAME/KEY: misc feature
/ LOCATION: (7415)..(7494)
/ OTHER INFORMATION: U5
/ NAME/KEY: misc feature
/ LOCATION: (7154)..(7165)
/ OTHER INFORMATION: PPT
/ NAME/KEY: misc feature
/ LOCATION: (388)..(391)
/ OTHER INFORMATION: splice donor (AGGT)
/ NAME/KEY: misc feature
/ LOCATION: (5074)..(5077)
/ OTHER INFORMATION: env splice acceptor (AGGC)
/ NAME/KEY: misc feature
/ LOCATION: (6982)..(6985)
/ OTHER INFORMATION: C1a1 splice acceptor (AGGA)
/ NAME/KEY: gene
/ LOCATION: (372)..(902)
/ OTHER INFORMATION: gag p19
/ NAME/KEY: gene
/ LOCATION: (909)..(1094)
/ OTHER INFORMATION: gag p10
/ NAME/KEY: gene
/ LOCATION: (1095)..(1814)
/ OTHER INFORMATION: gag p27
/ NAME/KEY: gene
/ LOCATION: (1843)..(2108)

```

```

; OTHER INFORMATION: gag p12
; NAME/KEY: gene
; LOCATION: (2109)..(2480)
; OTHER INFORMATION: gag p15
; NAME/KEY: misc_signal
; LOCATION: (2481)..(2483)
; OTHER INFORMATION: gag stop
; NAME/KEY: gene
; LOCATION: (2501)..(4216)
; OTHER INFORMATION: pol RT
; NAME/KEY: gene
; LOCATION: (4217)..(5185)
; OTHER INFORMATION: pol IN
; NAME/KEY: misc_signal
; LOCATION: (5186)..(5188)
; OTHER INFORMATION: pol stop
; NAME/KEY: gene
; LOCATION: (5244)..(6263)
; OTHER INFORMATION: env gp85
; NAME/KEY: gene
; LOCATION: (6264)..(6878)
; OTHER INFORMATION: env gp37
; NAME/KEY: misc_signal
; LOCATION: (6879)..(6881)
; OTHER INFORMATION: env stop
; NAME/KEY: misc_feature
; LOCATION: (7027)
; OTHER INFORMATION: ClaI site/ the ClaI site in gag is methylated in
; OTHER INFORMATION: Dam+ strains and does not cut
US-09-470-881-1

```

```

Query Match 74.6%; Score 390.2; DB 4; Length 11627;
Best Local Similarity 99.2%; Pred. No. 3.9e-129;
Matches 392; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 128 GCGATCTAGCGGCGAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGCGGAAG 187
Db 7034 GCGATGTAGCGGCGAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGCGGAAG 7093

Qy 188 CGGGGCTCGGTTGACGCGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGA 247
Db 7094 CGGGGCTCGGTTGACGCGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGA 7153

Qy 248 TAGGGAGGGGAAATAGTCTTATGCAATATCTCTTAGTCTTGCAACATGTTAGCAT 307
Db 7154 TAGGGAGGGGAAATAGTCTTATGCAATATCTCTTAGTCTTGCAACATGTTAGCAT 7213

Qy 308 GAGTTAGCAACATGCTTTACAGGAGAGAGAAAGCAGCGTGCATGCCGATTGTTGAAGT 367
Db 7214 GAGTTAGCAACATGCTTTACAGGAGAGAGAAAGCAGCGTGCATGCCGATTGTTGAAGT 7273

Qy 368 AAGTGTTACGATCGTGCCTTATAGGAGGCAACAGACGGGTCTGACATGGATTGGACG 427
Db 7274 AAGTGTTACGATCGTGCCTTATAGGAGGCAACAGACGGGTCTGACATGGATTGGACG 7333

Qy 428 AACCATTAATTCGCAATCGCAGATATGTTATTAAGTGCCTAGCTCGATCAATATA 487
Db 7334 AACCATTAATTCGCAATCGCAGATATGTTATTAAGTGCCTAGCTCGATCAATATA 7393

Qy 488 CGCCATTGACCATTCACCATTTGGTGTGCACCT 522
Db 7394 CGCCATTGACCATTCACCATTTGGTGTGCACCT 7428

```

```

RESULT 59
US-08-972-218-2
; Sequence 2, Application US/08972218
; Patent No. 6197502
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.

```

```

; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE
; TITLE OF INVENTION: DISCOVERY, CHARACTERIZATION AND ISOLATION OF GENES
; TITLE OF INVENTION: ENCODING POLYPEPTIDES WITH A PREDETERMINED PROPERTY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008358-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-972-218-2

```

```

Query Match 39.2%; Score 205.2; DB 3; Length 9521;
Best Local Similarity 98.6%; Pred. No. 8.5e-63;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 261 ATGTAGTCTTATGCAATATCTTGTAGTCTTGCAACATGTTAGTGTAGTGTAGCAT 320
Db 664 ATTCAGTCTTATGCAATATCTTGTAGTCTTGCAACATGTTAGTGTAGTGTAGCAT 723

Qy 321 GCCTTACAGGAGAGAGAAAGCAGCGTGCATGCCGATTGTTGGAAGTGTAGCAT 380
Db 724 GCCTTACAGGAGAGAGAAAGCAGCGTGCATGCCGATTGTTGGAAGTGTAGCAT 783

Qy 381 CGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGAACCAACCAATTC 440
Db 784 CGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGAACCAACCAATTC 843

Qy 441 CGCATTCGAGAGATATTTGTTTAAAGTGC 470
Db 844 CGCATTCGAGAGATATTTGTTTAAAGTGC 873

```

```

RESULT 60
US-09-193-707-2
; Sequence 2, Application US/09193707
; Patent No. 6524792
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY,
; TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WITH
; TITLE OF INVENTION: A PREDETERMINED PROPERTY
; FILE REFERENCE: 8358-0005-999

```

```

1  RESULT 62
2  US-801-092-5
3  / Sequence 5, Application US/08801092
4  / Patent No. 6074850
5  / GENERAL INFORMATION:
6  / APPLICANT: Antelman, Douglas
7  / APPLICANT: Gregory, Richard J.
8  / APPLICANT: Wals, Kenneth N.
9  / TITLE OF INVENTION: Tissue Specific Expression of
10 / TITLE OF INVENTION: Retinoblastoma Protein
11 / NUMBER OF SEQUENCES: 46
12 / CORRESPONDENCE ADDRESS:
13 / ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
14 / STREET: Two Embarcadero Center, 8th Floor
15 / CITY: San Francisco
16 / STATE: CA
17 / COUNTRY: USA
18 / ZIP: 94111
19 / COMPUTER READABLE FORM:
20 / MEDIUM TYPE: Floppy disk
21 / COMPUTER: IBM PC compatible
22 / OPERATING SYSTEM: PC-DOS/MS-DOS
23 / SOFTWARE: PatentIn Release #1.0, Version #1.30
24 / CURRENT APPLICATION DATA:
25 / APPLICATION NUMBER: US/08/801,092
26 / FILING DATE: 14-FEB-1997
27 / CLASSIFICATION: 514
28 / PRIOR APPLICATION DATA:
29 / APPLICATION NUMBER: US 08/751,517

```

```

/ CLASSIFICATION: 514
/
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: Fitts, Renee A.
/
/ REGISTRATION NUMBER: 35,136
/
/ REFERENCE/DOCKET NUMBER: 016930-001020
/
/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: 415-576-0200
/
/ TELEFAX: 703-576-0300
/
/ INFORMATION FOR SEQ ID NO: 5:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 383 base pairs
/
/ TYPE: nucleic acid
/
/ STRANDEDNESS: single
/
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: DNA (genomic)
/
/ FEATURE:
/
/ NAME/KEY: CDS
/
/ LOCATION: 209..250
/
/ FEATURE:
/
/ NAME/KEY: CDS
/
/ LOCATION: 254..289

```

FEATURE:	NAME/KEY:	CDS
LOCATION:	LOCATION:	293..505
FEATURE:	NAME/KEY:	CDS
LOCATION:	LOCATION:	509..514
FEATURE:	NAME/KEY:	CDS
LOCATION:	LOCATION:	518..520
FEATURE:	NAME/KEY:	CDS
LOCATION:	LOCATION:	524..658
FEATURE:	NAME/KEY:	CDS
LOCATION:	LOCATION:	662..691
FEATURE:	NAME/KEY:	CDS
LOCATION:	LOCATION:	695..748
FEATURE:	NAME/KEY:	CDS
LOCATION:	LOCATION:	752..781
FEATURE:	NAME/KEY:	CDS
LOCATION:	LOCATION:	785..814

```

; NAME/KEY: CDS
; LOCATION: 785..829
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1132..1134
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1138..1149
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..862
;
US-08-801-092-5
Query Match      28.9%; Score 151.4; DB 3; Length 3853;
Best Local Similarity 99.3%; Pred. No. 1e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140
QY 61 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGTTAGCGTTTGGG 120
Db 141 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGTTAGCGTTTGGG 200
QY 121 CTGCTTCGGATGTACGGCCAGATATTCGGGT 153
Db 201 CTGCTTCGGATGTACGGCCAGATATATACGGGT 233

```

```

RESULT 63
US-09-315-113-5
; Sequence 5, Application US/09315113
; Patent No. 6379927
; GENERAL INFORMATION:
; APPLICANT: Atreman, Douglas
; Gregory, Richard J.
; Wilis, Kenneth N.
; TITLE OF INVENTION: Tissue Specific Expression of
; Retinoblastoma Protein
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,113
; FILING DATE: 19-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/801,092
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 016930-001020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 703-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 209..250
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 254..289
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 293..505
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 509..514
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 518..520
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 524..658
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 662..691
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 695..748
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 752..781
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 785..829
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1132..1134
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1138..1149
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..862
;
US-09-315-113-5
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match      28.9%; Score 151.4; DB 4; Length 3853;
Best Local Similarity 99.3%; Pred. No. 1e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140
QY 61 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGTTAGCGTTTGGG 120
Db 141 ACAAGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGTTAGCGTTTGGG 200
QY 121 CTGCTTCGGATGTACGGCCAGATATTCGGGT 153
Db 201 CTGCTTCGGATGTACGGCCAGATATATACGGGT 233

RESULT 64
US-09-011-745-9
; Sequence 9, Application US/09011745
; Patent No. 6165715
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary KL
; APPLICANT: Weiss, Robin A
; APPLICANT: Takeuchi, Yasuhiro
; APPLICANT: Cosset, Francois-Loic
; TITLE OF INVENTION: Expression systems
; FILE REFERENCE: 09/011,745
; CURRENT APPLICATION NUMBER: US/09/011,745
; CURRENT FILING DATE: 1998-06-22

```

```

; EARLIER APPLICATION NUMBER: PCT/GB96/02061
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: GB9517263.1
; EARLIER FILING DATE: 1995-08-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 3925
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Portion of
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3910)
; OTHER INFORMATION: n is any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3911)
; OTHER INFORMATION: n is any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3912)
; OTHER INFORMATION: n is any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3913)
; OTHER INFORMATION: n is any nucleotide
; US-09-011-745-9

```

```

Query Match      28.9%; Score 151.4; DB 3; Length 3925;
Best Local Similarity 99.3%; Pred. No. 1.1e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db 70 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 129

QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGTTAGCGTTTTCG 120
Db 130 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGTTAGCGTTTTCG 189

QY 121 CTGCTTCGGGATGTACGGCGCCAGATATTCGGGT 153
Db 190 CTGCTTCGGGATGTACGGCGCCAGATATTCGGGT 222

```

```

RESULT 65
US-08-801-092-19
; Sequence 19, Application US/08801092
; Patent No. 6074850
; GENERAL INFORMATION:
; APPLICANT: Antelman, Douglas
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wills, Kenneth N.
; TITLE OF INVENTION: Tissue Specific Expression of
; TITLE OF INVENTION: Retinoblastoma Protein
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,092

```

```

; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/751,517
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 016930-001020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 703-576-0300
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4026 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 209..250
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 254..289
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 293..505
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 509..514
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 518..520
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 524..658
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 662..691
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 695..748
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 752..781
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 785..829
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 833..862
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1305..1307
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1311..1322
; US-08-801-092-19

```

```

Query Match      28.9%; Score 151.4; DB 3; Length 4026;
Best Local Similarity 99.3%; Pred. No. 1.1e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGTTAGCGTTTTCG 120
Db 141 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGTTAGGTTAGCGTTTTCG 200

```

QY 121 CTGCTCGCATGACGGCCAGATATTCGGGT 153  
Db 201 CTGCTCGCATGACGGCCAGATATTCGGGT 233

## RESULT 66

US-09-315-113-19  
; Sequence 19, Application US/09315113  
; Patent No. 6379927  
; GENERAL INFORMATION:  
; APPLICANT: Antelman, Douglas  
; Gregory, Richard J.  
; Wils, Kenneth N.  
; TITLE OF INVENTION: Tissue Specific Expression of  
; Retinoblastoma Protein  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/315,113  
; FILING DATE: 19-May-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/801,092  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 016930-001020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 703-576-0300  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4026 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 209..250  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 254..289  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 293..505  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 509..514  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 518..520  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 524..658  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 662..691  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 695..748

; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 752..781  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 785..829  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 833..862  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1305..1307  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1311..1322  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-315-113-19  
Query Match . 28.9%; Score 151.4; DB 4; Length 4026;  
Best Local Similarity 99.3%; Pred. No. 1.1e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTTGTTGGAGTCTGATGATGCTGCGGAGCAAAATTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTTGTTGGAGTCTGATGATGCTGCGGAGCAAAATTAAGCTACA 140  
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTAGGTTAGCGTTTTCG 120  
Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTAGGTTAGCGTTTTCG 200  
QY 121 CTGCTCGCATGACGGCCAGATATTCGGGT 153  
Db 201 CTGCTCGCATGACGGCCAGATATTCGGGT 233  
RESULT 67  
US-08-801-092-33  
; Sequence 33, Application US/08801092  
; Patent No. 6074850  
; GENERAL INFORMATION:  
; APPLICANT: Antelman, Douglas  
; APPLICANT: Gregory, Richard J.  
; APPLICANT: Wils, Kenneth N.  
; TITLE OF INVENTION: Tissue Specific Expression of  
; RETINOBLASTOMA PROTEIN  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/801,092  
; FILING DATE: 14-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/751,517  
; FILING DATE: 15-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 016930-001020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 703-576-0300

```

; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4249 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 209..250
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 254..289
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 293..505
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 509..514
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 518..520
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 524..658
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 662..691
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 695..748
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 752..781
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 785..829
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 833..862
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1528..1530
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1534..1545
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1548..1550
;
; US-08-801-092-33

```

```

Query Match      28.9%; Score 151.4; DB 3; Length 4249;
Best Local Similarity 99.3%; Pred No. 1.1e-43;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGTTGTTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGTTGTTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGCTTGCACGACATTCGATGAGATCTGCTAGGTTAGCGTTTTCG 120
Db 141 ACAAGGCAAGCTTGCACGACATTCGATGAGATCTGCTAGGTTAGCGTTTTCG 200

QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCGT 153
Db 201 CTGCTTCGCGATGTACGGGCGAGATATTCGCGT 233

```

```

RESULT 68
US-09-315-113-33
; Sequence 33, Application US/09315113
; Patent No. 6379927
; GENERAL INFORMATION:
;   APPLICANT: Antelman, Douglas
;               Gregory, Richard J.
;               Wills, Kenneth N.

```

```

; TITLE OF INVENTION: Tissue Specific Expression of
; Retinoblastoma Protein
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,113
; FILING DATE: 19-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/801,092
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 016930-001020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 703-576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4249 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 209..250
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 254..289
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 293..505
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 509..514
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 518..520
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 524..658
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 662..691
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 695..748
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 752..781
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 785..829
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 833..862
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1528..1530
;   FEATURE:

```

; NAME/KEY: CDS  
; LOCATION: 1534..1545  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-315-113-33

Query Match 28.9%; Score 151.4; DB 4; Length 4249;  
Best Local Similarity 99.3%; Pred. No. 1.1e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTAAGCTACA 60  
Db |||||  
Qy 81 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTAAGCTACA 140  
Db |||||

Qy 61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTGGG 120  
Db |||||

Qy 141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTGGG 200  
Db |||||

Qy 121 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 153  
Db |||||

Qy 201 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 233  
Db |||||

RESULT 69  
US-09-311-784A-35  
; Sequence 35, Application US/09311784A  
; Patent No. 6534482  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epiimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; FILE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/09/311,784A  
; CURRENT FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: 1999-05-13  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 5053  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: vector pEP2  
US-09-311-784A-35

Query Match 28.9%; Score 151.4; DB 4; Length 5053;  
Best Local Similarity 99.3%; Pred. No. 1.2e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTAAGCTACA 60  
Db |||||

Qy 81 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTAAGCTACA 140  
Db |||||

Qy 61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTGGG 120  
Db |||||

Qy 141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTGGG 200  
Db |||||

Qy 121 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 153  
Db |||||

Qy 201 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 233  
Db |||||

RESULT 70  
US-08-799-569-1  
; Sequence 1, Application US/08799569  
; Patent No. 6133244  
; GENERAL INFORMATION:  
; APPLICANT: Michel, Marie-Louise  
; APPLICANT: Mancine, Maryline  
; TITLE OF INVENTION: Nucleotide Vector, Composition

; APPLICANT: Michel, Marie-Louise  
; APPLICANT: Mancine, Maryline  
; TITLE OF INVENTION: Nucleotide Vector, Composition  
; TITLE OF INVENTION: Containing Such Vector, and Vaccine for Immunization  
; TITLE OF INVENTION: Against Hepatitis  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/799,569  
; FILING DATE: 12-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/706,337  
; FILING DATE: 30-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/633,821  
; FILING DATE: 22-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/00483  
; FILING DATE: 27-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03495.0128-01000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5618 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-799-569-1

Query Match 28.9%; Score 151.4; DB 3; Length 5618;  
Best Local Similarity 99.3%; Pred. No. 1.3e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTAAGCTACA 60  
Db |||||

Qy 81 CTGCTCCCTGCTGTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTAAGCTACA 140  
Db |||||

Qy 61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTGGG 120  
Db |||||

Qy 141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTGGG 200  
Db |||||

Qy 121 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 153  
Db |||||

Qy 201 CTGCTTCGGATGTACGGGCCAGATATTCGGGT 233  
Db |||||

RESULT 71  
US-09-570-546-1  
; Sequence 1, Application US/09570546  
; Patent No. 6429201  
; GENERAL INFORMATION:  
; APPLICANT: Michel, Marie-Louise  
; APPLICANT: Mancine, Maryline  
; TITLE OF INVENTION: Nucleotide Vector, Composition



Containing Such Vector, and Vaccine for Immunization  
Against Hepatitis

NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunnen  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/570,546  
FILING DATE: 12-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/799,569  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/706,337  
FILING DATE: 30-AUG-1996  
APPLICATION NUMBER: US 08/633,821  
FILING DATE: 22-APR-1996  
APPLICATION NUMBER: FR 94/00483  
FILING DATE: 27-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0128-01000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (Genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-570-546-1

Query Match 28.9%; Score 151.4; DB 4; Length 5618;  
Best Local Similarity 99.3%; Pred. No. 1.3e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTGGC 120  
Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTGGC 200

Qy 121 CTGCTCGGATGTACGGCCAGATATTCGCGT 153  
Db 201 CTGCTCGGATGTACGGCCAGATATTCGCGT 233

RESULT 72  
US-09-146-072A-1  
Sequence 1, Application US/09146072A  
Patent No. 6635624  
GENERAL INFORMATION:  
APPLICANT: Davis, Heather L.  
APPLICANT: Whalen, Robert G.  
APPLICANT: Michel, Marie-Louise  
TITLE OF INVENTION: NUCLEOTIDE VECTOR, COMPOSITION CONTAINING SUCH VECTOR AND VACCINE  
FOR IMMUNIZATION AGAINST HEPATITIS

FILE REFERENCE: C01040.70004.US  
CURRENT APPLICATION NUMBER: US/09/146,072A  
CURRENT FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: US 08/633,821  
PRIOR FILING DATE: 1996-08-02  
PRIOR APPLICATION NUMBER: PCT/FR94/000483  
PRIOR FILING DATE: 1994-04-27  
PRIOR APPLICATION NUMBER: FR 93/12659  
PRIOR FILING DATE: 1993-10-22  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 1  
LENGTH: 5618  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-09-146-072A-1

Query Match 28.9%; Score 151.4; DB 4; Length 5618;  
Best Local Similarity 99.3%; Pred. No. 1.3e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTGGC 120  
Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTGGC 200

Qy 121 CTGCTCGGATGTACGGCCAGATATTCGCGT 153  
Db 201 CTGCTCGGATGTACGGCCAGATATTCGCGT 233

RESULT 73  
US-09-439-923-1  
Sequence 1, Application US/09439923  
Patent No. 6426208  
GENERAL INFORMATION:  
APPLICANT: Emil D. Kakkis  
APPLICANT: Becky Tanamachi  
TITLE OF INVENTION: Recombinant Alpha-L-Iduronidase, Methods  
for Producing and Purifying the Same and Methods for  
TITLE OF INVENTION: Treating Diseases Caused by Deficiencies Thereof  
FILE REFERENCE: 08000051US00  
CURRENT APPLICATION NUMBER: US/09/439,923  
CURRENT FILING DATE: 1999-11-12  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 6200  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1558) ... (3516)  
US-09-439-923-1

Query Match 28.9%; Score 151.4; DB 4; Length 6200;  
Best Local Similarity 99.3%; Pred. No. 1.4e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGGAGTCTGCTGAGTAGTGCAGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTGGC 120  
Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGTTAGGCGTTTGGC 200

Qy 121 CTGCTCGGATGTACGGCCAGATATTCGCGT 153

Db 201 CTGCTTCGGGATGTAAGCGGCCAGATATACGGGT 233  
|||||

## RESULT 74

US-09-711-205A-1  
; Sequence 1, Application US/09711205A  
; Patent No. 6585971  
; GENERAL INFORMATION:  
; APPLICANT: Emil D. Kakkis  
; APPLICANT: Becky Tanamachi  
; TITLE OF INVENTION: Recombinant Alpha-L-Ironidase, Methods  
; TITLE OF INVENTION: for Producing and Purifying the Same and Methods for  
; TITLE OF INVENTION: Treating Diseases Caused by Deficiencies Thereof  
; FILE REFERENCE: 0800051US00  
; CURRENT APPLICATION NUMBER: US/09/711,205A  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US/09/439,923  
; PRIOR FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 6200  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1558)...(3516)  
US-09-711-205A-1

Query Match 28.9%; Score 151.4; DB 4; Length 6200;  
Best Local Similarity 99.3%; Pred. No. 1.4e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 200  
QY 121 CTGCTTCGGGATGTACGGGCCAGATATACGGGT 153  
Db 201 CTGCTTCGGGATGTACGGGCCAGATATACGGGT 233

## RESULT 75

US-09-711-205A-1  
; Sequence 1, Application US/09711205A  
; Patent No. 6585971  
; GENERAL INFORMATION:  
; APPLICANT: Emil D. Kakkis  
; APPLICANT: Becky Tanamachi  
; TITLE OF INVENTION: Recombinant Alpha-L-Ironidase, Methods  
; TITLE OF INVENTION: for Producing and Purifying the Same and Methods for  
; TITLE OF INVENTION: Treating Diseases Caused by Deficiencies Thereof  
; FILE REFERENCE: 0800051US00  
; CURRENT APPLICATION NUMBER: US/09/711,205A  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US/09/439,923  
; PRIOR FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 6200  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1558)...(3516)  
US-09-711-205A-1

Query Match 28.9%; Score 151.4; DB 4; Length 6200;  
Best Local Similarity 99.3%; Pred. No. 1.4e-43;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTGGG 200  
QY 121 CTGCTTCGGGATGTACGGGCCAGATATACGGGT 153  
Db 201 CTGCTTCGGGATGTACGGGCCAGATATACGGGT 233

Search completed: March 11, 2004, 11:09:52  
Job time : 105.601 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 08:24:22 ; Search time 379.636 Seconds  
(without alignments)

5071.893 Million cell updates/sec

Title: US-09-733-368a-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgtccctcgtgtgtgtt.....accacattggtgcacctc 523

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2432557 seqs, 184079884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500.8	95.8	6836	14	US-10-331-329-18
2	500.8	95.8	8902	9	US-09-729-416A-1
3	500.8	95.8	9737	14	US-10-331-329-22
4	500.8	95.8	9737	14	US-10-331-329-23
5	500.8	95.8	9737	14	US-10-331-329-28
6	500.8	95.8	9871	14	US-10-331-329-24
7	500.8	95.8	10060	14	US-10-331-329-25
8	500.8	95.8	11265	14	US-10-185-318-1
9	500.8	95.8	11265	14	US-10-185-799-1
10	430.8	82.4	11600	9	US-09-847-101B-35
11	430.8	82.4	11600	10	US-09-482-682-49
12	430.8	82.4	11600	15	US-10-403-337-42
13	430.8	82.4	11600	15	US-10-351-890-42
14	393	75.1	8238	10	US-09-482-682-50
15	393	75.1	33622	15	US-10-403-337-44

Sequence 44, Appl  
Sequence 43, Appl  
Sequence 43, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 61, Appl  
Sequence 69, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 36, Appl  
Sequence 16, Appl  
Sequence 109, Appl  
Sequence 1, Appl  
Sequence 9, Appl  
Sequence 63, Appl  
Sequence 6, Appl  
Sequence 3, Appl  
Sequence 35, Appl  
Sequence 35, Appl  
Sequence 35, Appl  
Sequence 41, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 26, Appl  
Sequence 13, Appl  
Sequence 73, Appl  
Sequence 88, Appl  
Sequence 23, Appl  
Sequence 19, Appl  
Sequence 21, Appl  
Sequence 15, Appl  
Sequence 17, Appl  
Sequence 9, Appl  
Sequence 3, Appl  
Sequence 5, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 72, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 1, Appl  
Sequence 6, Appl  
Sequence 4, Appl  
Sequence 10, Appl  
Sequence 9, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 13, Appl  
Sequence 12, Appl  
Sequence 5, Appl  
Sequence 6, Appl  
Sequence 5, Appl  
Sequence 3, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 7, Appl  
Sequence 4, Appl  
Sequence 21, Appl  
Sequence 11, Appl  
Sequence 22, Appl  
Sequence 22, Appl  
Sequence 29, Appl

89 151.4 28.9 6595 14 US-10-126-764-29 Sequence 29, Appl  
90 151.4 28.9 6623 14 US-10-422-934-6 Sequence 6, Appl  
91 151.4 28.9 6639 14 US-10-422-934-12 Sequence 12, Appl  
92 151.4 28.9 6695 14 US-10-422-934-8 Sequence 8, Appl  
93 151.4 28.9 6695 14 US-10-422-934-14 Sequence 14, Appl  
94 151.4 28.9 6695 14 US-10-422-934-15 Sequence 15, Appl  
95 151.4 28.9 6746 14 US-10-422-934-5 Sequence 5, Appl  
96 151.4 28.9 6801 14 US-10-422-934-13 Sequence 13, Appl  
97 151.4 28.9 6801 14 US-10-422-934-16 Sequence 16, Appl  
98 151.4 28.9 6818 14 US-10-422-934-7 Sequence 7, Appl  
99 151.4 28.9 6828 14 US-10-422-934-1 Sequence 1, Appl  
100 151.4 28.9 6833 14 US-10-422-934-10 Sequence 10, Appl

# ALIGNMENTS

RESULT 1  
US-10-331-329-18  
; Sequence 18, Application US/10331329  
; Publication No. US20030180267A1  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003CON  
; CURRENT APPLICATION NUMBER: US/10/331,329  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: 09/276,820  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6836  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-331-329-18

Query Match 95.8%; Score 500.8; DB 14; Length 6836;  
Best Local Similarity 98.5%; Pred. No. 4.9e-162;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGTTCGCTGAGTGTGCGGAGCAAAATTAAGCTACA 60  
Db 1299 CTGCTCCCTGCTTGTGTGGAGTTCGCTGAGTGTGCGGAGCAAAATTAAGCTACA 1358  
QY 61 ACAAGCAAGGCTTGCACGACAAATTCATGAAGAACTCTGTAGGGTTAGGCGTTTTCG 120  
Db 1359 ACAAGCAAGGCTTGCACGACAAATTCATGAAGAACTCTGTAGGGTTAGGCGTTTTCG 1418  
QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 1419 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 1478  
QY 181 CGAAAGCGGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
Db 1479 CGCCACAGGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 1538  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
Db 1539 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCACTTGTAGTCTTGCACATGG 1598  
QY 301 TAACGATGAGTTAGCAACNTGCTTTACAAGGAGAGAAAGCAACCGTGATGCCGATTGG 360

Db 1599 TAACGATGAGTTAGCAACATGCTTTCAGAGAGAGAAAGCAACCGTGATGCCGATTGG 1658  
QY 361 TGGAGTAAAGTGTGATGATGCGTCTTATTAGGAAGCAACAGACGGTCTGACATGGA 420  
Db 1659 TGGAGTAAAGTGTGATGATGCGTCTTATTAGGAAGCAACAGACAGGTCTGACATGGA 1718  
QY 421 TTGACGAAACACCTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGTGCTAGCTCGAT 479  
Db 1719 TTGACGAAACACCTAAATTCGCAATTCGAGAT-ATTGTATTAAAGTGTGCTAGCTCGAT 1778  
QY 480 ACAATAAAGCGCAATTCACCAATTCACCAATTCGCTGTGCACCTC 523  
Db 1779 ACAATAAAGCGCAATTCACCAATTCACCAATTCGCTGTGCACCTC 1822

RESULT 2  
US-09-729-416A-1  
; Sequence 1, Application US/09729416A  
; Patent No. US20020055172A1  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; TITLE OF INVENTION: MULTIPLE PROMOTER EXPRESSION CONSTRUCTS AND METHODS OF  
; TITLE OF INVENTION: USE  
; FILE REFERENCE: 0221-0004C  
; CURRENT APPLICATION NUMBER: US/09/729,416A  
; CURRENT FILING DATE: 2000-12-05  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 8902  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
; OTHER INFORMATION: (PRIG-MPI)  
US-09-729-416A-1

Query Match 95.8%; Score 500.8; DB 9; Length 8902;  
Best Local Similarity 98.5%; Pred. No. 5.7e-162;  
Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 1 CTGCTCCCTGCTTGTGTGGAGTTCGCTGAGTGTGCGGAGCAAAATTAAGCTACA 60  
Db 3365 CTGCTCCCTGCTTGTGTGGAGTTCGCTGAGTGTGCGGAGCAAAATTAAGCTACA 3424  
QY 61 ACAAGCAAGGCTTGCACGACAAATTCATGAAGAACTCTGTAGGGTTAGGCGTTTTCG 120  
Db 3425 ACAAGCAAGGCTTGCACGACAAATTCATGAAGAACTCTGTAGGGTTAGGCGTTTTCG 3484  
QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 3485 CTGCTTCGCGATGTACGGGCGAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGG 3544  
QY 181 CGAAAGCGGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 240  
Db 3545 CGCCACAGGGGCTTCGGTTGACGGGTTAGGAGTCCCTCAGGATATAGTATTTCGC 3604  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCTCTGTAGTCTTGCACATGG 300  
Db 3605 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATCACTTGTAGTCTTGCACATGG 3664  
QY 301 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAGCAACCGTGATGCCGATTGG 360  
Db 3665 TAACGATGAGTTAGCAACATGCTTACAAGGAGAGAAAGCAACCGTGATGCCGATTGG 3724  
QY 361 TGGAGTAAAGTGTGATGATGCGTCTTATTAGGAAGCAACAGACGGTCTGACATGGA 420  
Db 3725 TGGAGTAAAGTGTGATGATGCGTCTTATTAGGAAGCAACAGACAGGTCTGACATGGA 3784  
QY 421 TTGACGAAACACCTAAATTCGCAATTCACCAATTCGCTGTGCACCTC 479  
Db 3785 TTGACGAAACACCTAAATTCGCAATTCACCAATTCGCTGTGCACCTC 3844

```

; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-23

      Query Match          95.8%; Score 500.8; DB 14; Length 9737;
      Best Local Similarity 98.5%; Pred. No. 5.9e-162;
      Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1   CTGCTCCCTCTGTTGCTGTGGAGGTGCGCTCAGTAGTGCGCGAGCAAAATTTAAGCTACA   60
Db      1152 CTGCTCCCTCTGTTGCTGTGGAGGTGCGCTCAGTAGTGCGCGAGCAAAATTTAAGCTACA   1211

QY      61   ACAAGGCAAGGCTTACCGCAAAATGTCATGAAGAATCTCTTTAGGGTTAGCGGTTTTGCG   120
Db      1212 ACAAGGCAAGGCTTACCGCAAAATGTCATGAAGAATCTCTTTAGGGTTAGCGGTTTTGCG   1271

QY      121   CTGCTTCGGCATGTACGGGCCAAGATATTCGCGGTATCTGAGGGGACTAGGGTGTGTTAGG   180
Db      1272 CTGCTTCGGCATGTACGGGCCAAGATATTCGCGGTATCTGAGGGGACTAGGGTGTGTTAGG   1331

QY      181   CGAAAAAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC   240
Db      1332 CGCCACAGCGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTTCAGGATATAGTAGTTTCGC   1391

QY      241   TTTTGCATAGGAGGGGGAATGTAGTCTTTATGCAATCTCTTGTAGCTCTTGCAACATGG   300

```

Db 1392 TTTTCCATAGGAGGGGAAATAGTCTTATGCATACACTTCTAGTCTTGCACATGG 1451  
QY 301 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGACCCGTCGATGCGATGG 360  
Db 1452 TTAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGACCCGTCGATGCGATGG 1511  
QY 361 TGAAGTAAAGTGTAGTACGATCGTCTTATTAGGAGGCAACAGCGGTCTGCATGGA 420  
Db 1512 TGAAGTAAAGTGTAGTACGATCGTCTTATTAGGAGGCAACAGCGGTCTGCATGGA 1571  
QY 421 TTGGACGAAACCACTTAAATCCGATTCGAGAGAT-ATTGTATTTTAAAGTCTAGCTCGAT 479  
Db 1572 TTGGACGAAACCACTTAAATCCGATTCGAGAGAT-ATTGTATTTTAAAGTCTAGCTCGAT 1631  
QY 480 ACAATAAGCCGATTCACCATTCACACATTCGTCGACCTC 523  
Db 1632 ACAATAAGCCGATTCACCATTCACACATTCGTCGACCTC 1675

## RESULT 5

US-10-331-329-28

; Sequence 28, Application US/10331329

; Publication No. US20030180267A1

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE REFERENCE: 0221-0003CON

; CURRENT APPLICATION NUMBER: US/10/331,329

; CURRENT FILING DATE: 2002-12-30

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 28

; LENGTH: 9737

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8347)

; OTHER INFORMATION: a, c, t, g, other or unknown

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8499)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-10-331-329-28

Query Match 95.8%; Score 500.8; DB 14; Length 9737;

Best Local Similarity 98.5%; Pred. No. 5.9e-162;

Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTGGCGAGCAAAATTTAAGCTACA 60

Db 1152 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTGGCGAGCAAAATTTAAGCTACA 1211

QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGTTAGCGCTTTTGG 120

Db 1212 ACAAGCAAGGCTTGACCGCAATTCGATGAAGATCTGTTAGGTTAGCGCTTTTGG 1271

QY 121 CTGCTCCGATGTAGCGGCGAGATTCGGGTATCTGAGGAGGACTAGGTGTGTAGG 180

Db 1272 CTGCTTCGCGATGTACGGGCCAGATATACGGTATCTGAGGGGACTAGGCTGTGTTAGG 1331  
QY 181 CGAAAGAGGGGGCTTGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTGG 240  
Db 1332 CGCCACAGGGGGCTTGGTTGTACGGGTTAGAGTCCCTCAGGATATAGTAGTTTGG 1391  
QY 241 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGG 300  
Db 1392 TTTTGCATAGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGG 1451  
QY 301 TAAAGTATAGTTACCAACATGCTTACAGGAGAGAAAAGACCCGTCGATGCGATGG 360  
Db 1452 TAAAGTATAGTTACCAACATGCTTACAGGAGAGAAAAGACCCGTCGATGCGATGG 1511  
QY 361 TGAAGTAAAGTGTAGTACGATCGTCTTATTAGGAGGCAACAGCGGTCTGCATGGA 420  
Db 1512 TGAAGTAAAGTGTAGTACGATCGTCTTATTAGGAGGCAACAGCGGTCTGCATGGA 1571  
QY 421 TTGGACGAAACCACTTAAATCCGATTCGAGAGAT-ATTGTATTTTAAAGTCTAGCTCGAT 479  
Db 1572 TTGGACGAAACCACTTAAATCCGATTCGAGAGAT-ATTGTATTTTAAAGTCTAGCTCGAT 1631  
QY 480 ACAATAAGCCGATTCACCATTCACACATTCGTCGACCTC 523  
Db 1632 ACAATAAGCCGATTCACCATTCACACATTCGTCGACCTC 1675

## RESULT 6

US-10-331-329-24

; Sequence 24, Application US/10331329

; Publication No. US20030180267A1

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE REFERENCE: 0221-0003CON

; CURRENT APPLICATION NUMBER: US/10/331,329

; CURRENT FILING DATE: 2002-12-30

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 9871

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8481)

; OTHER INFORMATION: a, c, t, g, other or unknown

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8633)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-10-331-329-24

Query Match 95.8%; Score 500.8; DB 14; Length 9871;

Best Local Similarity 98.5%; Pred. No. 6e-162;

Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTGGCGAGCAAAATTTAAGCTACA 60

Db 1286 CTGCTCCCTGCTGTGTGGAGGTGCGTGTAGTGGCGAGCAAAATTTAAGCTACA 1345

QY	61	ACNAGGCAAGGCTTGACCGCAANTTGCATGAGAATCTGCTTAGGCTTAGGCTTTTGGC	120
Db	1346	ACRAGGCAAGGCTTGACCGCAANTTGCATGAGAATCTGCTTAGGCTTAGGCTTTTGGC	1405
QY	121	CTGCTTCGGCATGTACGGGCCAGATATCTGCGTACTCTGAGGCGCATAGGGTGTGTTTAGG	180
Db	1406	CTGCTTCGGCATGTACGGGCCAGATATACGCGTATCTAGGGGCACTAGGGTGTGTTTAGG	1465
QY	181	CGAARAAGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC	240
Db	1466	CGCCACGCGGGGCTTCGGTTGTACGCGGTTAGGAGTCCCTCAGGATATAGTAGTTTGGC	1525
QY	241	TTTTGCATATAGGAGGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTTGCCAATCGG	300
Db	1526	TTTTGCATATAGGAGGGGGAAATGTAGTCTTATGCAATACACTTGTAGTCTTTGCCAATCGG	1585
QY	301	TACCATGCTGTAGCAACATCCCTTACAGGAGGAAAGACACGGTGCATCCGCTTTGG	360
Db	1586	TACCATGCTGTAGCAACATCCCTTACAGGAGGAAAGACACGGTGCATCCGCTTTGG	1645
QY	361	TGGAAGTAAAGTGGTACGATCGTCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGA	420
Db	1646	TGGAAGTAAAGTGGTACGATCGTCCCTTATTAGGAAGGCAACAGACAGGTCTGACATGGA	1705
QY	421	TTGAGCAAGCACCTAAATTCGGATTTGCGAGAGAT-ATTGTAATTAAAGTGCGTAGCTCGAT	479
Db	1706	TTGAGCAAGCACCTGAATTCGGATTTGCGAGAGATATTGTAATTAAAGTGCGTAGCTCGAT	1765
QY	480	ACAAATAAACGCCATTGTACCAATTCACCAANTGGTGTGCACCTC	523
Db	1766	ACAAATAAACGCCATTGTACCAATTCACCAANTGGTGTGCACCTC	1809

QY 1 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 110 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTGTGGCGGAGCAAAATTTAAGCTACA 169  
 QY 61 ACAAGCAAGCTGTGACCGCAATTTGATGAGAAATCTGCTTAGGGTTAGGGTTTGG 120  
 Db 170 ACAAGCAAGCTGTGACCGCAATTTGATGAGAAATCTGCTTAGGGTTAGGGTTTGG 229  
 QY 121 CTGCTCCGCGATGTACGGGCGAGATTTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 230 CTGCTCCGCGATGTACGGGCGAGATTTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 289  
 QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGCTTAGGGTCCCTCAGGATATAGTATTGCG 240  
 Db 290 CGCCAGCGGGGCTTCGGTTGTACGGGCTTAGGGTCCCTCAGGATATAGTATTGCG 349  
 QY 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGTGCAATGG 300  
 Db 350 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGTGCAATGG 409  
 QY 301 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAGCACCGTGCATGCGATTGG 360  
 Db 410 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAGCACCGTGCATGCGATTGG 469  
 QY 361 TGGAGTAAGTGTGATGATGCTGCTTTATTAAGAGGCAACAGACCGGTTGACATGGA 420  
 Db 470 TGGAGTAAGTGTGATGATGCTGCTTTATTAAGAGGCAACAGACCGGTTGACATGGA 529  
 QY 421 TTGAGCAACCACTAAATTCGCAATGCGATGAGAT-ATTGTATTTAAGTCTAGCTCGAT 479  
 Db 530 TTGAGCAACCACTAAATTCGCAATGCGATGAGAT-ATTGTATTTAAGTCTAGCTCGAT 589  
 QY 480 ACAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGTGCACCTC 523  
 Db 590 ACAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGTGCACCTC 633

RESULT 9  
 US-10-185-799-1  
 ; Sequence 1, Application US/10185799  
 ; Publication No. US20030072742A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOYLE, JEFFREY S.  
 ; APPLICANT: BRADY, JAMIE L.  
 ; APPLICANT: LEW, ANDREW M.  
 ; TITLE OF INVENTION: ENHANCEMENT OF IMMUNE RESPONSE USING TARGETING  
 ; TITLE OF INVENTION: MOLECULES  
 ; FILE REFERENCE: FIRC:009USCI  
 ; CURRENT APPLICATION NUMBER: US/10/185,799  
 ; CURRENT FILING DATE: 2002-06-28  
 ; PRIOR APPLICATION NUMBER: 09/402,020  
 ; PRIOR FILING DATE: 1999-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/AU98/00208  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: AU PP5891  
 ; PRIOR FILING DATE: 1997-03-27  
 ; PRIOR APPLICATION NUMBER: AU PP1830  
 ; PRIOR FILING DATE: 1998-02-13  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 1  
 ; TYPE: DNA  
 ; ORGANISM: Murine  
 US-10-185-799-1  
 Query Match 95.8%; Score 500.8; DB 14; Length 11265;  
 Best Local Similarity 98.5%; Pred. No. 6.4e-162;  
 Matches 516; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 110 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTGTGGCGGAGCAAAATTTAAGCTACA 169

QY 61 ACAAGCAAGCTGTGACCGCAATTTGATGAGAAATCTGCTTAGGGTTAGGGTTTGG 120  
 Db 170 ACAAGCAAGCTGTGACCGCAATTTGATGAGAAATCTGCTTAGGGTTAGGGTTTGG 229  
 QY 121 CTGCTCCGCGATGTACGGGCGAGATTTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 230 CTGCTCCGCGATGTACGGGCGAGATTTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 289  
 QY 181 CGAAAGCGGGGCTTCGGTTGTACGGGCTTAGGGTCCCTCAGGATATAGTATTGCG 240  
 Db 290 CGCCAGCGGGGCTTCGGTTGTACGGGCTTAGGGTCCCTCAGGATATAGTATTGCG 349  
 QY 241 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGTGCAATGG 300  
 Db 350 TTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATATCTTGTAGTCTTGTGCAATGG 409  
 QY 301 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAGCACCGTGCATGCGATTGG 360  
 Db 410 TAACGATGAGTTAGCAATGCTTACAGGAGAGAAAGCACCGTGCATGCGATTGG 469  
 QY 361 TGGAGTAAGTGTGATGATGCTGCTTTATTAAGAGGCAACAGACCGGTTGACATGGA 420  
 Db 470 TGGAGTAAGTGTGATGATGCTGCTTTATTAAGAGGCAACAGACCGGTTGACATGGA 529  
 QY 421 TTGAGCAACCACTAAATTCGCAATGCGATGAGAT-ATTGTATTTAAGTCTAGCTCGAT 479  
 Db 530 TTGAGCAACCACTAAATTCGCAATGCGATGAGAT-ATTGTATTTAAGTCTAGCTCGAT 589  
 QY 480 ACAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGTGCACCTC 523  
 Db 590 ACAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGTGCACCTC 633

RESULT 10  
 US-09-847-101B-35  
 ; Sequence 35, Application US/09847101B  
 ; Publication No. US20020193327A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VON SEGGERN, DANIEL  
 ; APPLICANT: NEMEROW, GLEN R.  
 ; APPLICANT: FRIEDLANDER, MARTIN  
 ; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER  
 ; FILE REFERENCE: 22908-1226B  
 ; CURRENT APPLICATION NUMBER: US/09/847,101B  
 ; CURRENT FILING DATE: 2001-05-01  
 ; PRIOR APPLICATION NUMBER: 09/562,934  
 ; PRIOR FILING DATE: 2000-05-01  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 35  
 ; LENGTH: 11600  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid MMIV-E2a-SV40-Neo  
 US-09-847-101B-35  
 Query Match 82.4%; Score 430.8; DB 9; Length 11600;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-137;  
 Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 11167 CTGCTCCCTGCTGTGTGGAGTGCCTGAGTGTGGCGGAGCAAAATTTAAGCTACA 11226  
 QY 61 ACAAGCAAGCTGTGACCGCAATTTGATGAGAAATCTGCTTAGGGTTAGGGTTTGG 120  
 Db 11227 ACAAGCAAGCTGTGACCGCAATTTGATGAGAAATCTGCTTAGGGTTAGGGTTTGG 11286  
 QY 121 CTGCTCCGCGATGTACGGGCGAGATTTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 180  
 Db 11287 CTGCTCCGCGATGTACGGGCGAGATTTCCGCTATCTGAGGGGACTAGGGTGTGTTAGG 11346



QY 181 CGAAAGGGGGCTTCGGTGTAGCGGTAGAGTCCCTCAGCATATAGTTCGC 240  
Db 11347 CGAAAGGGGGCTTCGGTGTAGCGGTAGAGTCCCTCAGCATATAGTTCGC 11406  
QY 241 TTTTCCATPAGGAGGGGAAATAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
Db 11407 TTTTCCATPAGGAGGGGAAATAGTCTTATGCAATCTTGTAGTCTTGCACATGG 11466  
QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 360  
Db 11467 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 11526  
QY 361 TGGAGTAAGTGTAGCACTCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 420  
Db 11527 TGGAGTAAGTGTAGCACTCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 11586  
QY 421 TTGGACGAACCACT 434  
Db 11587 TTGGACGAACCACT 11600

RESULT 11  
US-09-482-682-49  
; Sequence 49, Application US/09482682  
; Publication No. US20030157688A1  
; GENERAL INFORMATION:  
; APPLICANT: VON SEGGER, DANIEL  
; APPLICANT: NEMEROW, GLEN R.  
; APPLICANT: HALLENBECK, PAUL  
; APPLICANT: STEVENSON, SUSAN  
; APPLICANT: SKRIPCHENKO, YELENA  
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,  
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE  
; FILE REFERENCE: 1294.0010001  
; CURRENT FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 11600  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: plasmid  
US-09-482-682-49

Query Match 82.4%; Score 430.8; DB 10; Length 11600;  
Best Local Similarity 99.5%; Pred. No. 1.2e-137;  
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 11167 CTGCTCCCTGCTTGTGTGGAGTGGCTGAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 11167 CTGCTCCCTGCTTGTGTGGAGTGGCTGAGTGGCGGAGCAAAATTTAAGCTACA 11226  
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGATCTGTTAGGGTTAGGCGTTTGG 120  
Db 11227 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGATCTGTTAGGGTTAGGCGTTTGG 11286  
QY 121 CTGCTTCGCGATGACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 11287 CTGCTTCGCGATGACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 11346  
QY 181 CGAAAGCGGGGCTTCGGTGTAGCGGTTAGGATCCCTCAGCATATAGTATGTTGCG 240  
Db 11347 CGAAAGCGGGGCTTCGGTGTAGCGGTTAGGATCCCTCAGCATATAGTATGTTGCG 11406  
QY 241 TTTTGCATPAGGAGGGGAAATAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
Db 11407 TTTTGCATPAGGAGGGGAAATAGTCTTATGCAATCTTGTAGTCTTGCACATGG 11466  
QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 360  
Db 11467 TTTTGCATPAGGAGGGGAAATAGTCTTATGCAATCTTGTAGTCTTGCACATGG 11466  
QY 361 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 360  
Db 11527 TGGAGTAAGTGTAGCACTCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 420  
QY 421 TTGGACGAACCACT 434

Db 11467 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 11526  
QY 361 TGGAGTAAGTGTAGCACTCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 420  
Db 11527 TGGAGTAAGTGTAGCACTCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 11586  
QY 421 TTGGACGAACCACT 434  
Db 11587 TTGGACGAACCACT 11600

RESULT 12  
US-10-403-337-42  
; Sequence 42, Application US/10403337  
; Publication No. US20030215948A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Nemerow, Glen R.  
; APPLICANT: Smith, Theodore  
; APPLICANT: Stevenson, Susan C.  
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting  
; FILE REFERENCE: 22908-1236B  
; CURRENT APPLICATION NUMBER: US/10/403.337  
; CURRENT FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: 10/351,890  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 60/350,388  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/391,967  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patent In version 3.0  
; SEQ ID NO 42  
; LENGTH: 11600  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Neo  
US-10-403-337-42

Query Match 82.4%; Score 430.8; DB 15; Length 11600;  
Best Local Similarity 99.5%; Pred. No. 1.2e-137;  
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 11167 CTGCTCCCTGCTTGTGTGGAGTGGCTGAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 11167 CTGCTCCCTGCTTGTGTGGAGTGGCTGAGTGGCGGAGCAAAATTTAAGCTACA 11226  
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGATCTGTTAGGGTTAGGCGTTTGG 120  
Db 11227 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGATCTGTTAGGGTTAGGCGTTTGG 11286  
QY 121 CTGCTTCGCGATGACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 180  
Db 11287 CTGCTTCGCGATGACGGGCGAGATATTCGGGTATCTGAGGGGACTAGGGTGTGTTAGG 11346  
QY 181 CGAAAGCGGGGCTTCGGTGTAGCGGTTAGGATCCCTCAGCATATAGTATGTTGCG 240  
Db 11347 CGAAAGCGGGGCTTCGGTGTAGCGGTTAGGATCCCTCAGCATATAGTATGTTGCG 11406  
QY 241 TTTTGCATPAGGAGGGGAAATAGTCTTATGCAATCTTGTAGTCTTGCACATGG 300  
Db 11407 TTTTGCATPAGGAGGGGAAATAGTCTTATGCAATCTTGTAGTCTTGCACATGG 11466  
QY 301 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 360  
Db 11467 TAACGATGAGTTAGCAACATGCTTACAGGAGAGAAAGACCGTGCATGCCATGG 11526  
QY 361 TGGAGTAAGTGTAGCACTCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 420  
Db 11527 TGGAGTAAGTGTAGCACTCGTGCCTTATTAGGAGGCAACAGACGGTCTGCATGGA 11586  
QY 421 TTGGACGAACCACT 434

Db 11587 TTGACGACCACT 11600

RESULT 13

US-10-351-890-42  
; Sequence 42, Application US/10351890  
; Publication No. US20040002060A1  
; GENERAL INFORMATION:

; APPLICANT: Stevenson, Susan C.  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Smith, Theodore  
; APPLICANT: Nemerow, Glen R.

; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting

; CURRENT APPLICATION NUMBER: US/10/351,890

; FILE REFERENCE: 22908-1236

; CURRENT FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: 60/350,388

; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/391,967

; PRIOR FILING DATE: 2002-06-26

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 42

; LENGTH: 11600

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURES:

; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Neo

US-10-351-890-42

Query Match 82.4%; Score 430.8; DB 15; Length 11600;

Best Local Similarity 99.5%; Pred. No. 1.2e-137;

Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTTAAGTACA 60

Db 11167 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGAGCAAAATTTAAGTACA 11226

QY 61 ACAAGGCAAGGCTTACCGGCAATTCGATGAAGATCTCTTAGGGTTAGCGTTTGGC 120

Db 11227 ACAAGGCAAGGCTTACCGGCAATTCGATGAAGATCTCTTAGGGTTAGCGTTTGGC 11286

QY 121 CTGCTTCGCGATGTACGGGCGAGATATTCGGTATCTGAGGCGACTAGGCTGTGTAGG 180

Db 11287 CTGCTTCGCGATGTACGGGCGAGATATTCGGTATCTGAGGCGACTAGGCTGTGTAGG 11346

QY 181 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTCGC 240

Db 11347 CGAAAACGGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTCGC 11406

QY 241 TTTTTCATAGGAGGAGGGAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 300

Db 11407 TTTTTCATAGGAGGAGGGAATCTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGG 11466

QY 301 TAACCATGATGTAGCAATGCTTACAGGAGAGAAAAGCACCGTGATGCCATTTGG 360

Db 11467 TAACCATGATGTAGCAATGCTTACAGGAGAGAAAAGCACCGTGATGCCATTTGG 11526

QY 361 TGAAGTAAAGTGTGATCGTGTCTTATTAGGAGGCAACAGCGGGTCTGACATGGA 420

Db 11527 TGAAGTAAAGTGTGATCGTGTCTTATTAGGAGGCAACAGCGGGTCTGACATGGA 11586

QY 421 TTGAGGAAACCACT 434

Db 11587 TTGAGGAAACCACT 11600

RESULT 14

US-09-482-682-50  
; Sequence 50, Application US/09482682  
; Publication No. US20030157688A1  
; GENERAL INFORMATION:

; APPLICANT: VON SEGGERN, DANIEL  
; APPLICANT: NEMEROW, GLEN R.  
; APPLICANT: HALLENBECK, PAUL  
; APPLICANT: STEVENSON, SUSAN  
; APPLICANT: SKRIPCHENKO, YELENA

; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,  
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE

; FILE REFERENCE: 1294.0010001

; CURRENT APPLICATION NUMBER: US/09/482,682

; CURRENT FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 50

; LENGTH: 8238

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURES:

; OTHER INFORMATION: Description of Artificial Sequence: plasmid

US-09-482-682-50

Query Match 75.1%; Score 393; DB 10; Length 8238;

Best Local Similarity 98.8%; Pred. No. 1.2e-124;

Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGGCG 182

Db 404 GCGCCCCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGGTGTGTTAGGCG 463

QY 183 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTCGCTT 242

Db 464 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTATTCGCTT 523

QY 243 TTCCATAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTA 302

Db 524 TTGCTAGGAGGGGGAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTA 583

QY 303 ACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAAGCACCGTGATCCGATTGGTG 362

Db 584 ACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAAGCACCGTGATCCGATTGGTG 643

QY 363 GAAGTAAGTGTGATGATCTGCTGCTTATTAGGAGGCAACAGCGGTCTGCATGAT 422

Db 644 GAAGTAAGTGTGATGATCTGCTGCTTATTAGGAGGCAACAGCGGTCTGCATGAT 703

QY 423 GGAAGCAACCACTAAATCCCATTTGAGGAGAGATATTGTTAAGTGCTAGCTCGATACA 482

Db 704 GGAAGCAACCACTAAATCCCATTTGAGGAGAGATATTGTTAAGTGCTAGCTCGATACA 763

QY 483 ATAAAGCCCATTTGACCAATTCACCATTTGTTGCACTTC 523

Db 764 ATAAAGCCCATTTGACCAATTCACCATTTGTTGCACTTC 804

RESULT 15

US-10-403-337-44

; Sequence 44, Application US/10403337

; Publication No. US20030215948A1

; GENERAL INFORMATION:

; APPLICANT: Kaleko, Michael

; APPLICANT: Nemerow, Glen R.

; APPLICANT: Smith, Theodore

; APPLICANT: Stevenson, Susan C.

; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting

; FILE REFERENCE: 22908-1236B

; CURRENT APPLICATION NUMBER: US/10/403,337

; CURRENT FILING DATE: 2003-03-27

; PRIOR APPLICATION NUMBER: 10/351,890

; PRIOR FILING DATE: 2003-01-24

; PRIOR APPLICATION NUMBER: 60/350,388

; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/391,967

; PRIOR FILING DATE: 2002-06-26

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 33622  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid Av3nBg  
US-10-403-337-44

Query Match 75.1%; Score 393; DB 15; Length 33622;  
Best Local Similarity 98.8%; Pred. No. 2.5e-124;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 123 GCTTCGCATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
Db |||  
QY 183 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
Db |||  
QY 456 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 515  
Db |||  
QY 243 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGTA 302  
Db |||  
QY 303 ACCATGAGTTAGCAACATGCCCTTACAGGAGAGAAAAGCACCCTGCGATCCGATTGGTG 362  
Db |||  
QY 363 GAAGTAAAGTGTACGATCGCTTATAGGAGGAAAGCAAGAGCGGTCTGACATGGATT 422  
Db |||  
QY 423 GGACGAACCACTAAATTCGCGATTCAGAGATATTTGATTTAAGTGTAGTCTGCATACA 482  
Db |||  
QY 483 ATAAAGCCATTGACCAATTCACCAATTCGCTGTGCACCTC 523  
Db |||  
QY 523 ATAAAGCCATTGACCAATTCACCAATTCGCTGTGCACCTC 796  
Db |||

## RESULT 16

US-10-351-890-44  
; Sequence 44, Application US/10351890  
; Publication No. US2004002060A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Nemerow, Susan C.  
; APPLICANT: Smith, Theodore  
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting  
; FILE REFERENCE: 22908-1236  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: 60/350,388  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/391,967  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 33622  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid Av3nBg  
US-10-351-890-44

Query Match 75.1%; Score 393; DB 15; Length 33622;  
Best Local Similarity 98.8%; Pred. No. 2.5e-124;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGCATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
Db |||  
QY 183 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
Db |||  
QY 456 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 515  
Db |||  
QY 243 TTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGTA 302  
Db |||  
QY 303 ACCATGAGTTAGCAACATGCCCTTACAGGAGAGAAAAGCACCCTGCGATCCGATTGGTG 362  
Db |||  
QY 363 GAAGTAAAGTGTACGATCGCTTATAGGAGGAAAGCAAGAGCGGTCTGACATGGATT 422  
Db |||  
QY 423 GGACGAACCACTAAATTCGCGATTCAGAGATATTTGATTTAAGTGTAGTCTGCATACA 482  
Db |||  
QY 483 ATAAAGCCATTGACCAATTCACCAATTCGCTGTGCACCTC 523  
Db |||  
QY 523 ATAAAGCCATTGACCAATTCACCAATTCGCTGTGCACCTC 796  
Db |||

## RESULT 17

US-10-403-337-43  
; Sequence 43, Application US/10403337  
; Publication No. US20030215948A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Nemerow, Glen R.  
; APPLICANT: Smith, Theodore  
; APPLICANT: Stevenson, Susan C.  
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting  
; FILE REFERENCE: 22908-1236B  
; CURRENT APPLICATION NUMBER: US/10/403,337  
; CURRENT FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: 10/351,890  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 60/350,388  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/391,967  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 43  
; LENGTH: 35211  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid AvinBg  
US-10-403-337-43

Query Match 75.1%; Score 393; DB 15; Length 35211;  
Best Local Similarity 98.8%; Pred. No. 2.6e-124;  
Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGCATGTACGGGCCAGATATTCGCGTATCTGAGGGGACTAGGGTGTGTTAGGCG 182  
Db |||  
QY 183 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
Db |||  
QY 456 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 515  
Db |||  
QY 515 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 629  
Db |||  
QY 629 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 755  
Db |||  
QY 755 AAAAGCGGGCTTCGGTTGTACGGGTTAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 889  
Db |||

QY 303 ACAGTACGATAGCAACATCCCTTACAGGAGAGAAAGACACCCCTGCATGCCGATTTGGT 362  
 Db 690 ACAGTACGATAGCAACATCCCTTACAGGAGAGAAAGACACCCCTGCATGCCGATTTGGT 749  
 QY 363 GAAGTACGATAGCAACATCCCTTACAGGAGAGAAAGACACCCCTGCATGCCGATTTGGT 422  
 Db 750 GAAGTACGATAGCAACATCCCTTACAGGAGAGAAAGACACCCCTGCATGCCGATTTGGT 809  
 QY 423 GGACGACCACTAAATTCGCAATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATACA 482  
 Db 810 GGACGACCACTAAATTCGCAATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATACA 869  
 QY 483 ATAAAGCGCATTTGACCATTCACACATTTGGTGTGCACCTC 523  
 Db 870 ATAAAGCGCATTTGACCATTCACACATTTGGTGTGCACCTC 910

RESULT 18  
 US-10-351-890-43  
 ; Sequence 43, Application US/10351890  
 ; Publication No. US20040002060A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stevenson, Susan C.  
 ; APPLICANT: Kaleko, Michael  
 ; APPLICANT: Smith, Theodore  
 ; APPLICANT: Nemerow, Glen R.  
 ; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting  
 ; FILE REFERENCE: 22908-1236  
 ; CURRENT APPLICATION NUMBER: US/10/351,890  
 ; CURRENT FILING DATE: 2003-01-28  
 ; PRIOR APPLICATION NUMBER: 60/350,388  
 ; PRIOR FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: 60/391,967  
 ; PRIOR FILING DATE: 2002-06-26  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 43  
 ; LENGTH: 35211  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Plasmid AvinBg  
 US-10-351-890-43

Query Match 75.1%; Score 393; DB 15; Length 35211;  
 Best Local Similarity 98.8%; Pred. No. 2.6e-124;  
 Matches 396; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 123 GCTTCGGATGTAGGGCCAGATATTCGGTATCTGAGGGACTAGGGTGTGTTAGGCG 182  
 Db 510 GCGCCCCGATGTAGGGCCAGATATTCGGTATCTGAGGGACTAGGGTGTGTTAGGCG 569  
 QY 183 AAAACGGGGCTTCGGTGTAGCGGTTCAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 242  
 Db 570 AAAACGGGGCTTCGGTGTAGCGGTTCAGGAGTCCCTCAGGATATAGTAGTTTCGCTT 629  
 QY 243 TTGCATAGGGAGGGGAAATGAGTCTTATGCAATCTTTGATGCTTGCACATGTA 302  
 Db 630 TTGCATAGGGAGGGGAAATGAGTCTTATGCAATCTTTGATGCTTGCACATGTA 689  
 QY 303 ACAGTACGATAGCAACATCCCTTACAGGAGAGAAAGACACCCCTGCATGCCGATTTGGT 362  
 Db 690 ACAGTACGATAGCAACATCCCTTACAGGAGAGAAAGACACCCCTGCATGCCGATTTGGT 749  
 QY 363 GAAGTACGATAGCAACATCCCTTACAGGAGAGAAAGACACCCCTGCATGCCGATTTGGT 422  
 Db 750 GAAGTACGATAGCAACATCCCTTACAGGAGAGAAAGACACCCCTGCATGCCGATTTGGT 809  
 QY 423 GGACGACCACTAAATTCGCAATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATACA 482  
 Db 810 GGACGACCACTAAATTCGCAATTCGAGATATTTGATTTAAAGTGCCTAGCTCGATACA 869

QY 483 ATAAAGCGCATTTGACCATTCACACATTTGGTGTGCACCTC 523  
 Db 870 ATAAAGCGCATTTGACCATTCACACATTTGGTGTGCACCTC 910

RESULT 19  
 US-09-897-006-9  
 ; Sequence 9, Application US/09897006  
 ; Patent No. US20020106729A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bleck, Gregory  
 ; TITLE OF INVENTION: Expression Vectors  
 ; FILE REFERENCE: GALA-06415  
 ; CURRENT APPLICATION NUMBER: US/09/897,006  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: 60/215,851  
 ; PRIOR FILING DATE: 2000-07-03  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 5130  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-09-897-006-9

Query Match 52.8%; Score 276.2; DB 9; Length 5130;  
 Best Local Similarity 93.7%; Pred. No. 2.7e-84;  
 Matches 310; Conservative 0; Mismatches 18; Indels 3; Gaps 2;

QY 195 TCGGTGTACCGCGTTAGGAGTCCCTCAGATATAGTAGTTTCGCTTTTCATAGGGAG 254  
 Db 2260 TAGGGTGTGCTGCCAAGTCCCTCAGATATAGTAGTTTCGCTTTTCATAGGGAG 2319  
 QY 255 GGGGAAATGATCTTATGCAATCTCTTGTAGTCTTGCACATGTTAAACGATGAGTAG 314  
 Db 2320 GGGGAAATGATCTTATGCAATCTCTTGTAGTCTTGCACATGTTAAACGATGAGTAG 2379  
 QY 315 CAACATGCTTTACAGGAGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTGG 374  
 Db 2380 CAACATGCTTTACAGGAGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTGG 2439  
 QY 375 TAGCATCGTCTTATTTAGGAGGCAACAGACGGGTCTGCATGAGTTGGACGAACTACT 434  
 Db 2440 TAGCATCGTCTTATTTAGGAGGCAACAGACGGGTCTGCATGAGTTGGACGAACTACT 2499  
 QY 435 AAATTCCCGCATTCAGAGAT-ATTCTATTAAAGTGCCTAGCTCGATACAATAAAGCCCA- 492  
 Db 2500 GAATTCCCGCATTCAGAGAT-ATTCTATTAAAGTGCCTAGCTCGATACAATAAAGCCCA- 2559  
 QY 493 -TTTGACCATTCACCATTTGGTGTGCACCT 522  
 Db 2560 TTTTGACCATTCACCATTTGGTGTGCACCT 2590

RESULT 20  
 US-09-897-511A-9  
 ; Sequence 9, Application US/09897511A  
 ; Publication No. US20030092882A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bremel, Robert  
 ; APPLICANT: Miller, Linda  
 ; APPLICANT: Bleck, Gregory  
 ; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors  
 ; FILE REFERENCE: GALA-06416  
 ; CURRENT APPLICATION NUMBER: US/09/897,511A  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: 60/215,925  
 ; PRIOR FILING DATE: 2000-07-03  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9

1 LENGTH: 5130  
2 TYPE: DNA  
3 ORGANISM: Artificial Sequence  
4 FEATURE:  
5 OTHER INFORMATION: Synthetic  
6 US-09-897-51A-9  
7  
8 Query Match 52.8%; Score 276.2; DB 10; Length 5130;  
9 Best Local Similarity 93.7%; Pred. No. 2.2e-84;  
10 Matches 310; Conservative 0; Mismatches 18; Indels 3; Gaps 2;  
11  
12 QY 195 TCGTTGACGCGTTAGGAGTCCCTCAGGATATAGTATTGCTTTTGCATAGGAG 254  
13 Db 2260 TAGGCTGCTGCGCACTGCATCCCTCAGGATATAGTATTGCTTTTGCATAGGAG 2319  
14  
15 QY 255 GGGGAATGATGCTTATCACTCTTGTAGTCTTGCAACATGGAAGATGATTAG 314  
16 Db 2320 GGGGAATGATGCTTATCACTCTTGTAGTCTTGCAACATGGAAGATGATTAG 2379  
17  
18 QY 315 CAACATGCTTTACAGGAGAGAAAAGCAGCGTGCATGCGATTGGTGAAGTAAAGTGG 374  
19 Db 2380 CAACATGCTTTACAGGAGAGAAAAGCAGCGTGCATGCGATTGGTGAAGTAAAGTGG 2439  
20  
21 QY 375 TAGATCTGCTTTATAGGAAGCAAGACAGCGGCTTGAATGATGGAAGCAACCACT 434  
22 Db 2440 TAGATCTGCTTTATAGGAAGCAAGACAGCGGCTTGAATGATGGAAGCAACCACT 2499  
23  
24 QY 435 AAATTCGCATTGCAGAT-ATTGTATTAACTGCTAGCTGCATACATATAAGCCCA- 492  
25 Db 2500 GAATTCGCATTGCAGATATTGTATTAACTGCTAGCTGCATACATATAAGCCCA- 2559  
26  
27 QY 493 -TTTGACCAATTCACCACTTGTGTGCACCT 522  
28 Db 2560 TTTTGACCAATTCACCACTTGTGTGCACCT 2590

## RESULT 21

US-09-965-703-69  
1 Sequence 69, Application US/09965703  
2 Patent No. US20020119521A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Rohm and Haas Company  
5 APPLICANT: Palli, Subba Reddy  
6 APPLICANT: Kapitskaya, Marianna Zinovjevna  
7 APPLICANT: Cress, Dean Ervin  
8 TITLE OF INVENTION: No. US20020119521A1el Bcdysone Receptor-Based Inducible Gene Expre  
9 FILE REFERENCE: A01020B  
10 CURRENT APPLICATION NUMBER: US/09/965,703  
11 PRIOR FILING DATE: 2001-09-26  
12 PRIOR APPLICATION NUMBER: 60/191,355  
13 PRIOR FILING DATE: 2000-03-22  
14 PRIOR APPLICATION NUMBER: 60/269,799  
15 PRIOR FILING DATE: 2001-02-20  
16 PRIOR APPLICATION NUMBER: PCT/US01/09050  
17 PRIOR FILING DATE: 2001-03-21  
18 NUMBER OF SEQ ID NOS: 75  
19 SOFTWARE: Patent in version 3.1  
20 SEQ ID NO 69  
21 LENGTH: 262  
22 TYPE: DNA  
23 ORGANISM: Rous sarcoma virus  
24 FEATURE:  
25 NAME/KEY: misc feature  
26 OTHER INFORMATION: No. US20020119521A1el Sequence  
27 US-09-965-703-69

Query Match 49.2%; Score 257.2; DB 9; Length 262;  
Best Local Similarity 98.9%; Pred. No. 2.2e-78;  
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTAAGATGATTAGCAACAT 320  
Db 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTAAGATGATTAGCAACAT 60

QY 321 GCCTTACAGGAGAGAAAAGCAGCGTGCATGCGATTGGTGAAGTAAAGTAAATTC 380  
Db 61 GCCTTACAGGAGAGAAAAGCAGCGTGCATGCGATTGGTGAAGTAAAGTAAATTC 120  
QY 381 CGTGCCTTATTAGGAAGGCAACAGACGCGTCTGCATGATGGAACCACTAAATTC 440  
Db 121 CGTGCCTTATTAGGAAGGCAACAGACGCGTCTGCATGATGGAACCACTAAATTC 180  
QY 441 CGATTGCGAGATATTGTATTAAAGTGCCTAGTCTGCATACATAAAGCCATTGACCA 500  
Db 181 CGATTGCGAGATATTGTATTAAAGTGCCTAGTCTGCATACATAAAGCCATTGACCA 240  
QY 501 TTCACCACATTTGGTGTGCACCT 522  
Db 241 TTCACCACATTTGGTGTGCACCT 262

## RESULT 22

US-10-239-134-61  
1 Sequence 61, Application US/10239134  
2 Publication No. US20040033600A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Rohm and Haas Company  
5 APPLICANT: Palli, Subba Reddy  
6 APPLICANT: Kapitskaya, Marianna Zinovjevna  
7 APPLICANT: Cress, Dean Ervin  
8 TITLE OF INVENTION: No. US20040033600A1el Bcdysone Receptor-Based Inducible Gene Expre  
9 FILE REFERENCE: RH0020  
10 CURRENT APPLICATION NUMBER: US/10/239,134  
11 PRIOR FILING DATE: 2002-09-19  
12 PRIOR APPLICATION NUMBER: 60/191,355  
13 PRIOR FILING DATE: 2000-03-22  
14 PRIOR APPLICATION NUMBER: 60/269,799  
15 PRIOR FILING DATE: 2001-02-20  
16 NUMBER OF SEQ ID NOS: 64  
17 SOFTWARE: Patent in version 3.0  
18 SEQ ID NO 61  
19 LENGTH: 262  
20 TYPE: DNA  
21 ORGANISM: Artificial Sequence  
22 FEATURE:  
23 NAME/KEY: misc feature  
24 OTHER INFORMATION: No. US20040033600A1el Sequence  
25 US-10-239-134-61

Query Match 49.2%; Score 257.2; DB 12; Length 262;  
Best Local Similarity 98.9%; Pred. No. 2.2e-78;  
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTAAGATGATTAGCAACAT 320  
Db 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTAAGATGATTAGCAACAT 60  
QY 321 GCCTTACAGGAGAGAAAAGCAGCGTGCATGCGATTGGTGAAGTAAAGTAAATTC 380  
Db 61 GCCTTACAGGAGAGAAAAGCAGCGTGCATGCGATTGGTGAAGTAAAGTAAATTC 120  
QY 381 CGTGCCTTATTAGGAAGGCAACAGACGCGTCTGCATGATGGAACCACTAAATTC 440  
Db 121 CGTGCCTTATTAGGAAGGCAACAGACGCGTCTGCATGATGGAACCACTAAATTC 180  
QY 441 CGATTGCGAGATATTGTATTAAAGTGCCTAGTCTGCATACATAAAGCCATTGACCA 500  
Db 181 CGATTGCGAGATATTGTATTAAAGTGCCTAGTCTGCATACATAAAGCCATTGACCA 240  
QY 501 TTCACCACATTTGGTGTGCACCT 522  
Db 241 TTCACCACATTTGGTGTGCACCT 262

## RESULT 23

US-10-155-736A-1

```

; Sequence 1, Application US/10155736A
; Publication No. US20030095948A1
; GENERAL INFORMATION:
; APPLICANT: Universit. di Torino
; TITLE OF INVENTION: Vector and methods of use for selective expression of genes in vivo
; TITLE OF INVENTION: Vector and methods of use for selective expression of genes in vivo
; FILE REFERENCE: 36019/MNN
; CURRENT APPLICATION NUMBER: US/10/155,736A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: -
; SEQ ID NO 1
; LENGTH: 10469
; TYPE: DNA
; ORGANISM: HIV-1
; US-10-155-736A-1

Query Match 41.6%; Score 217.4; DB 14; Length 10469;
Best Local Similarity 99.1%; Pred. No. 9.4e-64;
Matches 229; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 260 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGATGAACGATGATTAGCAACA 319
Db 2218 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGATGAACGATGATTAGCAACA 2277
QY 320 TGCCTTACAGGAGAGAAAACACCGTGCATGCCGATGCTGGAAGTAAGTGGTACGA 379
Db 2278 TGCCTTACAGGAGAGAAAACACCGTGCATGCCGATGCTGGAAGTAAGTGGTACGA 2337
QY 380 TGTGCGCTTATTAGGAAGCAACAGACGGGTCTGACATGCGATTGGACGAACCACTAAATT 439
Db 2338 TGTGCGCTTATTAGGAAGCAACAGACGGGTCTGACATGCGATTGGACGAACCACTAAATT 2397
QY 440 -CGCATTCGACAGATATTGTTATTTAAGTCGCTTACGATACATAAAG 489
Db 2398 GCGCATTCGACAGATATTGTTATTTAAGTCGCTTACGATACATAAAG 2448

RESULT 24
US-09-733-042-1
; Sequence 1, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; APPLICANT: Hennecke, Wolfgang A.
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.01.00001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 11282
; TYPE: DNA
; ORGANISM: pCvYts
; US-09-733-042-1

Query Match 39.2%; Score 205.2; DB 9; Length 11282;
Best Local Similarity 98.6%; Pred. No. 1.6e-59;
Matches 207; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 261 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGCTGTAACGATGATTAGCAACAT 320
Db 664 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGCTGTAACGATGATTAGCAACAT 723
QY 321 GCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATGCTGGAAGTAAGTGGTACGAT 380
Db 724 GCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATGCTGGAAGTAAGTGGTACGAT 783

```

Query Match	35.9%	Score 187.6;	DB 11;	Length 5283;
Best Local Similarity	91.5%;	Pred. No. 1.4e-53;		
Matches 214;	Conservative 0;	Mismatches 9;	Indels 11;	Gaps 1;
QY	300	GTAAAGCATGAGTTAGCAACATGCTTACAAGGAGAGAAAAAGCACCGTGCATCCGAGTGG	359	
Db	252	GTAAAGGTGAGTTAGCACATGCTTTATAGGAGAGAAAGCAGCGTGCATCCGAGTGG	311	
QY	360	GTGGAAAGTAAG-----GTGGTAGATCGTGTGCTTTATAGGAAGCAACAGACGG	408	
Db	312	GTGGAGTAAGGTGGTATGATCGGTGTATGATCGTGTGCTTTATAGGAAGCAACAGACGG	371	
QY	409	GTCGTACATCGATTGGAGACACCACTAAATTCGCCGATTCGACAGATATCTGTTAAAGTG	468	
Db	372	GTCCTAACCGGATTGGAGACACCACTGAATTCGCCGATTCGACAGATATCTGTTAAAGTG	431	
QY	469	CCTAGCTCGATACATAAAGCCATTGACCACTTCCACATCTGGTGTGACCT	522	
Db	432	CCCAGCTCGATACATAAAGCCATTGACCACTTCCACATCTGGTGTGACCT	485	

RESULT 27  
US-10-182-327-16  
; Sequence 16, Application US/10182327  
; Publication No. US20040043468A1  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: THE NEUROSCIENCE INSTITUTE  
; APPLICANT: MAURO, Vincent P.  
; APPLICANT: EDELMAN, Gerald M.  
; APPLICANT: CHAPPELL, Stephen A.  
; APPLICANT: OWENS, Geoffrey  
; APPLICANT: PINKSTAFF, Jason K.  
; APPLICANT: KRUSHAL, Leslie  
; APPLICANT: ZHOU, Wei  
; TITLE OF INVENTION: SYNTHETIC INTERNAL RIBOSOME ENTRY SITES AND METHODS OF IDENTIFYING  
; FILE REFERENCE: SCRIPI360-1  
; CURRENT APPLICATION NUMBER: US/10/182,327  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: PCT/US 01/02586  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/261,312  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/230,956  
; PRIOR FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: US 60/230,852  
; PRIOR FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: US 60/207,804  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: US 60/186,496  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 60/178,816  
; PRIOR FILING DATE: 2000-01-28  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16  
; LENGTH: 6250  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VECTOR  
US-10-182-327-16

Db	3224	ATGCGTCTTACAGGAGAGAAAAGCCGCTGCATCCGATTGGTGAAGTAAAGGTGTACG	3283
Qy	379	ATCGTGCCTTATTAGCAAGGCAACAGACGGGTCTGCATCGGATTGGACGACCACTTAAT	438
Db	3284	ATGCGTGCCTTATTAGCAAGGCAACAGACAGGTCTGCATGGATTGGACGAAACCACTGAT	3343
RESULT 28			
	US-10-182-329-109		
	Sequence 109, Application US/10182329		
	Publication No. US20040005564A1		
	GENERAL INFORMATION:		
	APPLICANT: THE SCRIPPS RESEARCH INSTITUTE		
	APPLICANT: MAURO, Vincent P.		
	APPLICANT: EDELMAN, Gerald M.		
	APPLICANT: CHAPPELL, Stephen A.		
	APPLICANT: JONES, Frederick S.		
	APPLICANT: OWENS, Geoffrey		
	APPLICANT: MEECH, Robin		
	TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRAN		
	TITLE OF INVENTION: REGULATORY ELEMENTS, AND COMPOSITIONS RELATING TO SAME		
	FILE REFERENCE: SCRIP1380-1		
	CURRENT APPLICATION NUMBER: US/10/182,329		
	CURRENT FILING DATE: 2001-01-26		
	PRIOR APPLICATION NUMBER: PCT/US 01/02733		
	PRIOR FILING DATE: 2001-01-26		
	PRIOR APPLICATION NUMBER: US 60/261,312		
	PRIOR FILING DATE: 2001-01-12		
	PRIOR APPLICATION NUMBER: US 60/230,956		
	PRIOR FILING DATE: 2000-09-07		
	PRIOR APPLICATION NUMBER: US 60/230,852		
	PRIOR FILING DATE: 2000-09-07		
	PRIOR APPLICATION NUMBER: US 60/207,804		
	PRIOR FILING DATE: 2000-05-30		
	PRIOR APPLICATION NUMBER: US 60/186,496		
	PRIOR FILING DATE: 2000-03-02		
	PRIOR APPLICATION NUMBER: US 60/178,816		
	PRIOR FILING DATE: 2000-01-28		
	NUMBER OF SEQ ID NOS: 112		
	SOFTWARE: PatentIn version 3.0		
	SEQ ID NO 109		
	LENGTH: 6250		
	TYPE: DNA		
	ORGANISM: Artificial sequence		
	FEATURE:		
	OTHER INFORMATION: vector		
	US-10-182-329-109		

	Query Match	33.5%;	Score 175.2;	DB 12;	Length 6250;
	Best Local Similarity	98.3%;	Pred. No. 3e-49;		
	Matches 177;	Conservative	0;	Mismatches 3;	Indels 0;
	Gaps	0;			
QY	259	AAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGTTACCAATGAGTTAGCAAC	318		
DB	3164	AAATGTAGTCTTATGCAATCTCTTGTAGTCTTGCAACATGTTACCAATGAGTTAGCAAC	3223		
QY	319	ATGCCTTTACAAGGAGAGAAAAACCGTGATCGCCGATTGTGTGAAGTAAAGTGTGATCG	378		

```

; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/230,852
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,816
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 8513
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: vector
US-10-182-329-9

Query Match      33.3%; Score 174.2; DB 15; Length 8513;
Best Local Similarity 95.7%; Pred. No. 7,8e-49;
Matches 179; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      248  TAGGAGAGGGGAAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGGTAAACGAT 307
Db      191  TGGCAAGCTAGAAATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGGTAAACGAT 250
QY      308  GAGTTAGCAACATGCCCTTACAAGGAGAGAAAAAGCACCGTGCATCCCGATTGGTGGAAAGT 367
Db      251  GAGTTAGCAACATGCCCTTACAGGAGAGAAAAAGCACCGTGCATCCCGATTGGTGGAAAGT 310
QY      368  AAGGTGGTACATCGTCGCTTATTAGAAAGGCAACAGACGGTCTGCATGGATTGGACG 427
Db      311  AAGGTGGTACATCGTCGCTTATTAGAAAGGCAACAGACGGTCTGCATGGATTGGACG 370
QY      428  AACCACT 434
Db      371  AACCACT 377

RESULT 31
US-10-264-237-633
; Sequence 633, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 633
; LENGTH: 766
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (91)..(91)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:

```



```

; NAME/KEY: misc feature
; LOCATION: (141)..(141)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (652)..(652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (753)..(753)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (763)..(763)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-633

Query Match      30.8%; Score 161.2; DB 15; Length 766;
Best Local Similarity 89.6%; Pred. No. 7e-45;
Matches 199; Conservative 0; Mismatches 10; Indels 13; Gaps 2;

QY 314 GCACATGCGCTTACAAGGAGAGAAAAAGCACCGTCATGCGGATTGGTGGAAAGTAA-CGT 372
DB 9 GCACATGCGCTTATAGGAGAGAAAGACCGTCATGCGGATTGGGAGGAGTAAGGGT 68

QY 373 GGTAGATCGTG-----CCTTATTAGGAAGCAACAGACGGGTCTGACATGGA 420
DB 69 GGTATGATCGTGTATGATGTCGTCCTTTGTAGGAAGCAACAGACGGGTCTAACACGGA 128

QY 421 TTGGACCAACCACTAATTCGGCATTCAGAGATATTCTATTAAAGTCCTAGCTCGATA 480
DB 129 TTGGACCAACCACTAATTCGGCATTCAGAGATATTCTATTAAAGTCCTAGCTCGATA 188

QY 481 CAATAAAGCGCAATTGACCAATTCACCACTTGTGTGCACT 522
DB 189 CAATAAAGCGCAATTGACCAATTCACCACTTGTGTGCACT 230

RESULT 32
US-10-205-534-6
; Sequence 6, Application US/10205534
; Publication No. US20030118601A1
; GENERAL INFORMATION:
; APPLICANT: Neill, James
; APPLICANT: Rigby, Mark
; APPLICANT: Jarrett, James
; TITLE OF INVENTION: FIV VACCINE
; FILE REFERENCE: 9013.10
; CURRENT APPLICATION NUMBER: US/10/205,534
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: US/09/380,990
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 9704977.9
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 1070
; TYPE: DNA
; ORGANISM: Petalumna strain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1070)
; OTHER INFORMATION: Sati-Sati Fragment in plasmid CMV Del. RT.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)..(896)
; OTHER INFORMATION: CMV promoter from pCDNA3 (a BglII - KpnI restriction fragment).
; NAME/KEY: misc feature
; LOCATION: (918)..(1070)
; OTHER INFORMATION: FIV genome from the t-RNA primer binding site to the viral SstI s

```

```

US-10-205-534-6

Query Match      28.9%; Score 151.4; DB 14; Length 1070;
Best Local Similarity 99.3%; Pred. No. 2.1e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 77 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 136

QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTCTTAGGGTTAGCGTTTTCG 120
DB 137 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTCTTAGGGTTAGCGTTTTCG 196

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCCGCT 153
DB 197 CTGCTTCGCGATGTACGGGCCAGATATTACCGCT 229

RESULT 33
US-10-277-184-3
; Sequence 3, Application US/10277184
; Publication No. US20030114406A1
; GENERAL INFORMATION:
; APPLICANT: Chen, William
; TITLE OF INVENTION: HYALURONIC ACID MICROSPHERES FOR
; FILE REFERENCE: 2055/1G717-US1
; CURRENT APPLICATION NUMBER: US/10/277,184
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/596,665
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 60/140,260
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4597
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCDNA3.1/BS vector by Invitrogen Corporation
US-10-277-184-3

Query Match      28.9%; Score 151.4; DB 14; Length 4597;
Best Local Similarity 99.3%; Pred. No. 4.5e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY 61 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTCTTAGGGTTAGCGTTTTCG 120
DB 141 ACAAGCAAGGCTTGACCGCAATTCGATGAAGAATCTCTTAGGGTTAGCGTTTTCG 200

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCCGCT 153
DB 201 CTGCTTCGCGATGTACGGGCCAGATATTACCGCT 233

RESULT 34
US-10-371-069-35
; Sequence 35, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.

```

```
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 5053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pep2
US-10-371-069-35

Query Match      28.9%; Score 151.4; DB 15; Length 5053;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAGAGATCTCTTAGGGTTAGCGGTTTGGC 120
DB 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAGAGATCTCTTAGGGTTAGCGGTTTGGC 200

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153
DB 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 35
US-10-371-645-35
; Sequence 35, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 5053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pep2
US-10-371-645-35

Query Match      28.9%; Score 151.4; DB 15; Length 5053;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAGAGATCTCTTAGGGTTAGCGGTTTGGC 120
DB 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAGAGATCTCTTAGGGTTAGCGGTTTGGC 200

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153
DB 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 35
US-10-371-645-35
; Sequence 35, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 5053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pep2
US-10-371-645-35

Query Match      28.9%; Score 151.4; DB 15; Length 5053;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAGAGATCTCTTAGGGTTAGCGGTTTGGC 120
DB 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAGAGATCTCTTAGGGTTAGCGGTTTGGC 200

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153
DB 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 36
US-10-371-260-35
; Sequence 35, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 5053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pep2
US-10-371-260-35

Query Match      28.9%; Score 151.4; DB 15; Length 5053;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
DB 81 CTGCTCCCTGCTGTGTGTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAGAGATCTCTTAGGGTTAGCGGTTTGGC 120
DB 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAGAGATCTCTTAGGGTTAGCGGTTTGGC 200

QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153
DB 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 37
US-09-795-006A-41
; Sequence 41, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalia et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
```

; PRIOR APPLICATION NUMBER: US 60/205,331  
 ; PRIOR FILING DATE: 2000-05-18  
 ; PRIOR APPLICATION NUMBER: US 60/185,205  
 ; PRIOR FILING DATE: 2000-02-25  
 ; NUMBER OF SEQ ID NOS: 175  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 41  
 ; LENGTH: 5070  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: pSectagi  
 ; OTHER INFORMATION: Vector  
 US-09-795-006A-41

Query Match 28.9%; Score 151.4; DB 9; Length 5070;  
 Best Local Similarity 99.3%; Pred. No. 4.7e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGACAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGACAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 120  
 Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 200  
 QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153  
 Db 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 38  
 US-09-815-981-13  
 ; Sequence 13, Application US/09815981  
 ; Publication No. US20030003435A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: de Jong, Gary  
 ; APPLICANT: Vanderbyl, Sandra  
 ; APPLICANT: Drayer, Jan  
 ; APPLICANT: Tak, Paul Peter  
 ; TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID  
 ; FILE REFERENCE: 24601-416  
 ; CURRENT APPLICATION NUMBER: US/09/815,981  
 ; CURRENT FILING DATE: 2001-03-22  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 5162  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Chimeric bacterial plasmid  
 US-09-815-981-13

Query Match 28.9%; Score 151.4; DB 10; Length 5162;  
 Best Local Similarity 99.3%; Pred. No. 4.7e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGACAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGACAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 120  
 Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 200  
 QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153  
 Db 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 39  
 US-09-815-979-13

; Sequence 13, Application US/09815979  
 ; Publication No. US200300059940A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: de Jong, Gary  
 ; APPLICANT: Vanderbyl, Sandra  
 ; APPLICANT: Perez, Carl  
 ; APPLICANT: Hoekstra, Richard  
 ; APPLICANT: Volker, Oberle  
 ; TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID  
 ; FILE REFERENCE: 24601-416  
 ; CURRENT APPLICATION NUMBER: US/09/815,979  
 ; CURRENT FILING DATE: 2001-03-22  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 5162  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Chimeric bacterial plasmid  
 US-09-815-979-13

Query Match 28.9%; Score 151.4; DB 10; Length 5162;  
 Best Local Similarity 99.3%; Pred. No. 4.7e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGACAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGACAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 120  
 Db 141 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 200  
 QY 121 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 153  
 Db 201 CTGCTTCGCGATGTACGGGCCAGATATTCGCGT 233

RESULT 40  
 US-10-235-119-13  
 ; Sequence 13, Application US/10235119  
 ; Publication No. US20030113917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: de Jong, Gary  
 ; APPLICANT: Vanderbyl, Sandra  
 ; APPLICANT: Drayer, Jan  
 ; APPLICANT: Tak, Paul Peter  
 ; TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID  
 ; FILE REFERENCE: 24601-416D  
 ; CURRENT APPLICATION NUMBER: US/10/235,119  
 ; CURRENT FILING DATE: 2002-09-03  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 5162  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Chimeric bacterial plasmid  
 US-10-235-119-13

Query Match 28.9%; Score 151.4; DB 14; Length 5162;  
 Best Local Similarity 99.3%; Pred. No. 4.7e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGACAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTTGTGTGGAGGTGCTGAGTAGTGGCGGACAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGGCTTGACCGCAATTCATGAGATCTGCTTAGGTTAGCGTTTTCGG 120

```

Db      141 ACAAGCAAGGCTTACCGACAAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 200
Qy      121 CTGCTTCGGCATGTACGGGCCAGATATTCGGCT 153
Db      201 CTGCTTCGGCATGTACGGGCCAGATATTCGGCT 233

RESULT 41
US-10-161-403-26
; Sequence 26, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 5162
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric bacterial plasmid
US-10-161-403-26

```

```

Query Match      28.9%; Score 151.4; DB 14; Length 5162;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CTGCTCCCTGCTGCTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db      81 CTGCTCCCTGCTGCTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140
Qy      61 ACAAGCAAGGCTTACCGACAAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 120
Db      141 ACAAGCAAGGCTTACCGACAAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 200
Qy      121 CTGCTTCGGCATGTACGGGCCAGATATTCGGCT 153
Db      201 CTGCTTCGGCATGTACGGGCCAGATATTCGGCT 233

```

```

RESULT 42
US-10-086-745-13
; Sequence 13, Application US/10086745
; Publication No. US20030186390A1
; GENERAL INFORMATION:
; APPLICANT: Vandebyl, Sandra
; APPLICANT: de Jong, Gary
; TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID
; FILE REFERENCE: 24601-416C
; CURRENT APPLICATION NUMBER: US/10/086,745
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5162
; TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric bacterial plasmid
US-10-086-745-13

Query Match      28.9%; Score 151.4; DB 14; Length 5162;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CTGCTCCCTGCTGCTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60
Db      81 CTGCTCCCTGCTGCTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140
Qy      61 ACAAGCAAGGCTTACCGACAAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 120
Db      141 ACAAGCAAGGCTTACCGACAAATTCATGAGAAATCTGTTAGGCTTAGCGCTTTTGG 200
Qy      121 CTGCTTCGGCATGTACGGGCCAGATATTCGGCT 153
Db      201 CTGCTTCGGCATGTACGGGCCAGATATTCGGCT 233

```

```

RESULT 43
US-10-005-876A-73
; Sequence 73, Application US/10005876A
; Publication No. US20030186233A1
; GENERAL INFORMATION:
; APPLICANT: Chesnut, Jonathan D.
; APPLICANT: Carrino, John
; APPLICANT: Leong, Louis
; APPLICANT: Madden, Knut
; APPLICANT: Gleeson, Martin
; APPLICANT: Fan, James
; APPLICANT: Brasch, Michael A.
; APPLICANT: Cheo, David
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; APPLICANT: Temple, Gary F.
; TITLE OF INVENTION: Methods and Compositions for Synthesis of Nucleic Acid
; FILE REFERENCE: 0942,5340002
; CURRENT APPLICATION NUMBER: US/10/005,876A
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/254,510
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,972
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/318,902
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/326,092
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/333,124
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 09/732,914
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 5173
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of plasmid pCDNA6.2/V5/GWD-TOPO
; NAME/KEY: unsure
; LOCATION: (958)..(966)
; OTHER INFORMATION: "n" can be any nucleotide: a, t, c, g
US-10-005-876A-73

```

```

Query Match      28.9%; Score 151.4; DB 14; Length 5173;
Best Local Similarity 99.3%; Pred. No. 4.7e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGCTTAGGCGTTTGGG 120  
Db 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGCTTAGGCGTTTGGG 200  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTTCGCGT 153  
Db 201 CTGCTTCGCGATGTACGGGCCAGATATTTCGCGT 233

## RESULT 44

US-10-161-403-88  
; Sequence 88, Application US/10161403  
; Publication No. US20030119104A1  
; GENERAL INFORMATION:  
; APPLICANT: Perkins, Edward  
; APPLICANT: Perez, Carl  
; APPLICANT: Lindenbaum, Michael  
; APPLICANT: Greene, Amy  
; APPLICANT: Leung, Josephine  
; APPLICANT: Fleming, Elena  
; APPLICANT: Stewart, Sandra  
; APPLICANT: Shellard, Joan  
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS  
; FILE REFERENCE: 24601-420  
; CURRENT APPLICATION NUMBER: US/10/161,403  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/294,758  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: 60/366,891  
; PRIOR FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88  
; LENGTH: 5192  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pIRSpuro2 plasmid from Clontech  
US-10-161-403-88

Query Match 28.9%; Score 151.4; DB 14; Length 5192;  
Best Local Similarity 99.3%; Pred. No. 4.7e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGCTTAGGCGTTTGGG 120  
Db 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGCTTAGGCGTTTGGG 200  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTTCGCGT 153  
Db 201 CTGCTTCGCGATGTACGGGCCAGATATTTCGCGT 233

## RESULT 45

US-09-826-115-23  
; Sequence 23, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; FILE REFERENCE: 14114.033203  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: pct/us99/12298

; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 5271  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; NAME/KEY: CDS  
; LOCATION: (910)...(2953)  
US-09-826-115-23

Query Match 28.9%; Score 151.4; DB 10; Length 5271;  
Best Local Similarity 99.3%; Pred. No. 4.8e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGCTTAGGCGTTTGGG 120  
Db 141 ACAAGGCAAGGCTTGACCGGCAATTCGATGAAGATCTGCTTAGGCTTAGGCGTTTGGG 200  
QY 121 CTGCTTCGCGATGTACGGGCCAGATATTTCGCGT 153  
Db 201 CTGCTTCGCGATGTACGGGCCAGATATTTCGCGT 233

## RESULT 46

US-09-826-115-19  
; Sequence 19, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; FILE REFERENCE: 14114.033203  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: pct/us99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 5283  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; NAME/KEY: CDS  
; LOCATION: (910)...(2965)  
US-09-826-115-19

Query Match 28.9%; Score 151.4; DB 10; Length 5283;  
Best Local Similarity 99.3%; Pred. No. 4.8e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTTGGAGTTCGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 120  
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 200  
QY 121 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 153  
Db 201 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 233

## RESULT 47

US-09-826-115-21  
; Sequence 21, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; FILE REFERENCE: 14114.0332U3  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: pct/us99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 5304  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; NAME/KEY: CDS  
; LOCATION: (910)...(2986)  
US-09-826-115-21

Query Match 28.9%; Score 151.4; DB 10; Length 5304;  
Best Local Similarity 99.3%; Pred. No. 4.8e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 60  
Db 81 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 140  
QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 120  
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 200  
QY 121 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 153  
Db 201 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 233

## RESULT 48

US-09-826-115-15  
; Sequence 15, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; FILE REFERENCE: 14114.0332U3  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: pct/us99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04

; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 5308  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; NAME/KEY: CDS  
; LOCATION: (911)...(2987)  
; NAME/KEY: misc feature  
; LOCATION: (1)...(5308)  
; OTHER INFORMATION: pCBWN  
US-09-826-115-15

Query Match 28.9%; Score 151.4; DB 10; Length 5308;  
Best Local Similarity 99.3%; Pred. No. 4.8e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 60  
Db 81 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 140  
QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 120  
Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTGCTAGGTTAGCGCTTTTGG 200  
QY 121 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 153  
Db 201 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 233

## RESULT 49

US-09-826-115-17  
; Sequence 17, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; FILE REFERENCE: 14114.0332U3  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: pct/us99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 5334  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; NAME/KEY: CDS  
; LOCATION: (916)...(3007)  
; NAME/KEY: misc feature  
; LOCATION: (1)...(5334)  
; OTHER INFORMATION: pCBJE 1-14  
US-09-826-115-17

Query Match 28.9%; Score 151.4; DB 10; Length 5334;  
Best Local Similarity 99.3%; Pred. No. 4.8e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 60  
Db 81 CTGCTCCGCTTGATGAGGCGGCGAGATATTCGGT 140

QY 61 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 200  
 Db |||||  
 QY 121 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 153  
 Db |||||  
 QY 201 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 233  
 Db |||||

RESULT 50  
 US-09-794-975-9  
 ; Sequence 9, Application US/09794975  
 ; Patent No. US20010034884A1  
 ; FILING DATE: 27-Apr-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIORITY INFORMATION:  
 ; APPLICATION NUMBER: US 08/759,505  
 ; FILING DATE: 04-DEC-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Frommer, William S.  
 ; REGISTRATION NUMBER: 25,506  
 ; REFERENCE/DOCKET NUMBER: 454312-2450  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 840-3333  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5446 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-09-844-645-3

Query Match 28.9%; Score 151.4; DB 9; Length 5432;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 153  
 Db |||||  
 QY 81 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 233  
 Db |||||  
 QY 61 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 200  
 Db |||||  
 QY 121 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 153  
 Db |||||  
 QY 201 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 233  
 Db |||||

RESULT 51  
 US-09-844-645-3  
 ; Sequence 3, Application US/09844645  
 ; Patent No. US2002010242A1  
 ; FILING DATE: 27-Apr-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIORITY INFORMATION:  
 ; APPLICATION NUMBER: US 08/759,505  
 ; FILING DATE: 04-DEC-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Frommer, William S.  
 ; REGISTRATION NUMBER: 25,506  
 ; REFERENCE/DOCKET NUMBER: 454312-2450  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 840-3333  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5446 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-09-844-645-3

QY 61 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 200  
 Db |||||  
 QY 121 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 153  
 Db |||||  
 QY 201 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 233  
 Db |||||

Query Match 28.9%; Score 151.4; DB 9; Length 5446;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 153  
 Db |||||  
 QY 81 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 233  
 Db |||||  
 QY 61 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 200  
 Db |||||  
 QY 121 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 153  
 Db |||||  
 QY 201 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 233  
 Db |||||

RESULT 52  
 US-09-559-874-5  
 ; Sequence 5, Application US/09559874  
 ; Publication No. US20020192726A1  
 ; FILING DATE: 27-Apr-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIORITY INFORMATION:  
 ; APPLICATION NUMBER: US 08/759,505  
 ; FILING DATE: 04-DEC-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Frommer, William S.  
 ; REGISTRATION NUMBER: 25,506  
 ; REFERENCE/DOCKET NUMBER: 454312-2450  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 840-3333  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5446 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-09-559-874-5

Query Match 28.9%; Score 151.4; DB 9; Length 5446;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 153  
 Db |||||  
 QY 81 CTGCTCCGCGATGTACGGGCCAGATATTCGGCT 233  
 Db |||||  
 QY 61 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 120  
 Db |||||  
 QY 141 ACAAGGCAAGCTTGCACGACAATTGCATGAAGAATCTGCTTAGGTTAGCGTTTTCGG 200  
 Db |||||

QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153  
 Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233

RESULT 53

US-10-371-116A-1  
 ; Sequence 11, Application US/10371116A  
 ; Publication No. US20040005589A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.  
 ; TITLE OF INVENTION: METHODS OF TREATMENT OR PREVENTION OF AUTOIMMUNE DISEASES  
 ; FILE REFERENCE: 87534-3900  
 ; CURRENT APPLICATION NUMBER: US/10/371,116A  
 ; PRIOR FILING DATE: 2003-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/227, 853  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 5446  
 ; TYPE: DNA  
 ; ORGANISM: artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: pcDNA3 vector nucleotide sequence  
 US-10-371-116A-1

Query Match 28.9%; Score 151.4; DB 15; Length 5446;

Best Local Similarity 99.3%; Pred. No. 4.9e-41;

Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60  
 Db 81 CTGCTCCCTGCTGTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTCTTAGGTTAGCGTTTTCGG 120

Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTCTTAGGTTAGCGTTTTCGG 200

QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153

Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233

RESULT 54

US-09-912-436-11  
 ; Sequence 11, Application US/09912436  
 ; Patent No. US20020068694A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JELTSCH, Markku M  
 ; APPLICANT: ALITALO, Kari  
 ; APPLICANT: OLOFSSON, Birgitta  
 ; APPLICANT: ERIKSSON, Ulf  
 ; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
 ; FILE REFERENCE: 1064-48929PV Markku JELTSCH et al  
 ; CURRENT APPLICATION NUMBER: US/09/912,436  
 ; CURRENT FILING DATE: 2001-07-26  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 5458  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: pSectaga-VEGF-BEX1-5-H6  
 US-09-912-436-11

Query Match

Best Local Similarity 28.9%; Score 151.4; DB 9; Length 5458;

Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60

Db 81 CTGCTCCCTGCTGTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTCTTAGGTTAGCGTTTTCGG 120

Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTCTTAGGTTAGCGTTTTCGG 200

QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153

Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233

RESULT 55

US-09-912-436-12  
 ; Sequence 12, Application US/09912436  
 ; Patent No. US20020068694A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JELTSCH, Markku M  
 ; APPLICANT: ALITALO, Kari  
 ; APPLICANT: OLOFSSON, Birgitta  
 ; APPLICANT: ERIKSSON, Ulf  
 ; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
 ; FILE REFERENCE: 1064-48929PV Markku JELTSCH et al  
 ; CURRENT APPLICATION NUMBER: US/09/912,436  
 ; CURRENT FILING DATE: 2001-07-26  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 12  
 ; LENGTH: 5458  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: pSectaga-VEGF-BEX1-5-H6-NXT  
 US-09-912-436-12

Query Match 28.9%; Score 151.4; DB 9; Length 5458;

Best Local Similarity 99.3%; Pred. No. 4.9e-41;

Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTCCCTGCTGTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 60

Db 81 CTGCTCCCTGCTGTGTGTGGAGGTCTGCTGAGTAGTGGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTCTTAGGTTAGCGTTTTCGG 120

Db 141 ACAAGCAAGGCTTGACCGCAATTCATGAAGAATCTCTTAGGTTAGCGTTTTCGG 200

QY 121 CTGCTCCGATGTACGGCCAGATATTCGGGT 153

Db 201 CTGCTCCGATGTACGGCCAGATATTCGGGT 233

RESULT 56

US-10-005-876A-72  
 ; Sequence 72, Application US/10005876A  
 ; Publication No. US20030186233A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chesnut, Jonathan D.  
 ; APPLICANT: Carrino, John  
 ; APPLICANT: Leong, Louis  
 ; APPLICANT: Madden, Knut  
 ; APPLICANT: Gleeson, Martin  
 ; APPLICANT: Fan, James  
 ; APPLICANT: Brasch, Michael A.  
 ; APPLICANT: Cheo, David  
 ; APPLICANT: Hartley, James L.  
 ; APPLICANT: Byrd, Devon R.N.  
 ; APPLICANT: Temple, Gary F.



;; TITLE OF INVENTION: Methods and Compositions for Synthesis of Nucleic Acid  
;; FILE REFERENCE: 0942.5340002  
;; CURRENT APPLICATION NUMBER: US/10/005,876A  
;; PRIOR FILING DATE: 2001-12-03  
;; PRIOR APPLICATION NUMBER: 60/254,510  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/291,972  
;; PRIOR FILING DATE: 2001-05-21  
;; PRIOR APPLICATION NUMBER: 60/318,902  
;; PRIOR FILING DATE: 2001-09-14  
;; PRIOR APPLICATION NUMBER: 60/326,092  
;; PRIOR FILING DATE: 2001-09-28  
;; PRIOR APPLICATION NUMBER: 60/333,124  
;; PRIOR FILING DATE: 2001-11-27  
;; PRIOR APPLICATION NUMBER: 09/732,914  
;; PRIOR FILING DATE: 2000-12-11  
;; NUMBER OF SEQ ID NOS: 80  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 72  
;; LENGTH: 5543  
;; TYPE: DNA  
;; ORGANISM: artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Nucleotide sequence of plasmid pCDNA3.2/V5/GW-D-TOPO  
;; NAME/KEY: unsure  
;; LOCATION: (958)..(966)  
;; OTHER INFORMATION: "n" can be any nucleotide: a, t, c, g  
US-10-005-876A-72

Query Match 28.9%; Score 151.4; DB 14; Length 5543;  
Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 200  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGGATGTACGGGCCAGATATTCGCGT 233

RESULT 57  
US-09-912-436-7  
; Sequence 7; Application US/09912436  
; Patent No. US20020068694A1  
; GENERAL INFORMATION:  
; APPLICANT: JELTSCH, Markku M  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ERIKSSON, Ulf  
; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
; FILE REFERENCE: AMOUNT OF SOLUBLE VEGF-B  
; FILE REFERENCE: 1064-48929PV Markku JELTSCH et al  
; CURRENT APPLICATION NUMBER: US/09/912,436  
; CURRENT FILING DATE: 2001-07-26  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 5614  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: pSectaga-VEGF-B167-H6  
US-09-912-436-7

Query Match 28.9%; Score 151.4; DB 9; Length 5614;  
Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 200  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGGATGTACGGGCCAGATATTCGCGT 233

RESULT 58  
US-09-912-436-8  
; Sequence 8; Application US/09912436  
; Patent No. US20020068694A1  
; GENERAL INFORMATION:  
; APPLICANT: JELTSCH, Markku M  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ERIKSSON, Ulf  
; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
; FILE REFERENCE: AMOUNT OF SOLUBLE VEGF-B  
; FILE REFERENCE: 1064-48929PV Markku JELTSCH et al  
; CURRENT APPLICATION NUMBER: US/09/912,436  
; CURRENT FILING DATE: 2001-07-26  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 5614  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: pSectaga-VEGF-B167-H6-NXT  
US-09-912-436-8

Query Match 28.9%; Score 151.4; DB 9; Length 5614;  
Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGTGGAGTTCGCTGAGTAGTGGCGAGCAAAATTTAAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTCGATGAAGAATCTGCTTAGGGTTAGCGCTTTTGG 200  
QY 121 CTGCTTCGGATGTACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGGATGTACGGGCCAGATATTCGCGT 233

RESULT 59  
US-10-142-358-1  
; Sequence 1; Application US/10142358  
; Publication No. US20030083291A1  
; GENERAL INFORMATION:  
; APPLICANT: Michel, Marie-Louise  
; APPLICANT: Mancine, Maryline  
; TITLE OF INVENTION: Nucleotide Vector, Composition  
; Containing Such Vector, and Vaccine for Immunization  
; Against Hepatitis  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; Turner

STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/142,358  
FILING DATE: 10-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/799,569  
FILING DATE: 12-FEB-1997  
APPLICATION NUMBER: US 08/706,337  
FILING DATE: 30-AUG-1996  
APPLICATION NUMBER: US 08/633,821  
FILING DATE: 22-APR-1996  
APPLICATION NUMBER: FR 94/00483  
FILING DATE: 27-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0128-01000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-142-358-1  
Query Match 28.9%; Score 151.4; DB 14; Length 5618;  
Best Local Similarity 99.3%; Pred. No. 4.9e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGCAAAATTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGCAAAATTAAGCTACA 140  
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGGTTAGCGGTTTGG 120  
Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGGTTAGCGGTTTGG 200  
QY 121 CTGCTTCGGATGACGGGCCAGATATTCGGGT 153  
Db 201 CTGCTTCGGATGACGGGCCAGATATTCGGGT 233  
RESULT 60  
US-09-780-933-6  
Sequence 6, Application US/09780933  
Patent No. US20020127652A1  
GENERAL INFORMATION:  
APPLICANT: SCHMAYE, HANS T.  
APPLICANT: ANDERSEN, KIM V.  
APPLICANT: VAN DEN HAZEL, BART  
APPLICANT: CHRISTIANSEN, JESPER  
APPLICANT: JEPPESEN, CLAUD B.  
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES  
FILE REFERENCE: 31-001000US  
CURRENT APPLICATION NUMBER: US/09/780,933  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: PA 2000 00220  
PRIOR FILING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: 60/184,035  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: PA 2000 01092  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,558  
PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 5651  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1231)..(1617)  
US-09-780-933-6  
Query Match 28.9%; Score 151.4; DB 9; Length 5651;  
Best Local Similarity 99.3%; Pred. No. 5e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGCAAAATTAAGCTACA 60  
Db 81 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGCAAAATTAAGCTACA 140  
QY 61 ACAAGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGGTTAGCGGTTTGG 120  
Db 141 ACAAGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGGTTAGCGGTTTGG 200  
QY 121 CTGCTTCGGATGACGGGCCAGATATTCGGGT 153  
Db 201 CTGCTTCGGATGACGGGCCAGATATTCGGGT 233  
RESULT 61  
US-09-896-896A-4  
Sequence 4, Application US/09896896A  
Publication No. US20030036181A1  
GENERAL INFORMATION:  
APPLICANT: MAXYGEN APS  
TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES  
FILE REFERENCE: 0217us210  
CURRENT APPLICATION NUMBER: US/09/896,896A  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/217,497  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: US 60/225,558  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: DK PA 2000 01027  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DK PA 2000 01092  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: PCT/DK00/00743  
PRIOR FILING DATE: 2000-12-29  
PRIOR APPLICATION NUMBER: PCT/DK01/00090  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 5651  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1231)..(1617)  
OTHER INFORMATION: Coding sequence for human FSH-beta  
US-09-896-896A-4  
Query Match 28.9%; Score 151.4; DB 10; Length 5651;  
Best Local Similarity 99.3%; Pred. No. 5e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTTGTGTGGAGGTCGCTGAGTAGTGGCGGCAAAATTAAGCTACA 60

Db 81 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTGGCGGACCAAAATTTAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 200  
QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 233

## RESULT 62

US-09-912-436-9  
; Sequence 9, Application US/09912436  
; Patent No. US20020068694A1  
; GENERAL INFORMATION:  
; APPLICANT: JELTSCH, Markku M  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ERIKSSON, Ulf  
; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
; FILE REFERENCE: 1064-48929PV Markku JELTSCH et al  
; CURRENT APPLICATION NUMBER: US/09/912,436  
; CURRENT FILING DATE: 2001-07-26  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5695  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: pSectaga-VEGF-B186-H6-NXT  
US-09-912-436-9

Query Match 28.9%; Score 151.4; DB 9; Length 5695;  
Best Local Similarity 99.3%; Pred. No. 5e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTGGCGGACCAAAATTTAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTGGCGGACCAAAATTTAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 200  
QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 233

## RESULT 63

US-09-912-436-10  
; Sequence 10, Application US/09912436  
; Patent No. US20020068694A1  
; GENERAL INFORMATION:  
; APPLICANT: JELTSCH, Markku M  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ERIKSSON, Ulf  
; TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCREASING THE  
; FILE REFERENCE: 1064-48929PV Markku JELTSCH et al  
; CURRENT APPLICATION NUMBER: US/09/912,436  
; CURRENT FILING DATE: 2001-07-26  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 5695  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: pSectaga-VEGF-B186-H6  
US-09-912-436-10

Query Match 28.9%; Score 151.4; DB 9; Length 5695;  
Best Local Similarity 99.3%; Pred. No. 5e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTGGCGGACCAAAATTTAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTGGCGGACCAAAATTTAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 200  
QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 233

## RESULT 64

US-09-765-555-66  
; Sequence 66, Application US/09765555  
; Publication No. US20030037355A1  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; TITLE OF INVENTION: Methods and compositions to modulate  
; FILE REFERENCE: 27801-20014.40  
; CURRENT APPLICATION NUMBER: US/09/765,555  
; PRIOR FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: US 09/620,897  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 60/177,468  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 5731  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: 2C7-SID  
US-09-765-555-66

Query Match 28.9%; Score 151.4; DB 10; Length 5731;  
Best Local Similarity 99.3%; Pred. No. 5e-41;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTGGCGGACCAAAATTTAGCTACA 60  
Db 81 CTGCTCCCTGCTGTGTGTGAGGTCGCTGAGTAGTGGCGGACCAAAATTTAGCTACA 140  
QY 61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 120  
Db 141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGATCTGCTTAGGTTAGCGGTTTGGC 200  
QY 121 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 153  
Db 201 CTGCTTCGCGATGACGGGCCAGATATTCGCGT 233

## RESULT 65

US-09-971-980-1  
; Sequence 1, Application US/09971980  
; Patent No. US20020164349A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, David B.  
; APPLICANT: Yang, Joo-Sung  
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruses

```

; TITLE OF INVENTION: Pestiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5864
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid
US-09-971-980-1

Query Match      28.9%; Score 151.4; DB 9; Length 5864;
Best Local Similarity 99.3%; Pred. No. 5.1e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGC 120
Db 141 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGC 200

Qy 121 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 153
Db 201 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 233

RESULT 66
US-09-971-980-4
; Sequence 4, Application US/09971980
; Patent No. US20020164349A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flavivirus
; TITLE OF INVENTION: Pestiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 5864
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid
US-09-971-980-4

Query Match      28.9%; Score 151.4; DB 9; Length 5864;
Best Local Similarity 99.3%; Pred. No. 5.1e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGC 120
Db 141 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGC 200

Qy 121 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 153
Db 201 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 233
```

```

RESULT 67
US-10-395-894-8
; Sequence 8, Application US/10395894
; Publication No. US20040033229A1
; GENERAL INFORMATION:
; APPLICANT: MADDON, Paul J.
; APPLICANT: DONOVAN, Gerald P.
; APPLICANT: OLSON, William C.
; APPLICANT: SCHLKE, No. US20040033229A1bert
; APPLICANT: GARDNER, Jason
; APPLICANT: MA, Dangshe
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
; FILE REFERENCE: P00741.70005.US
; CURRENT APPLICATION NUMBER: US/10/395,894
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: PCI/US02/33944
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/335,215
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/362,747
; PRIOR APPLICATION NUMBER: US 60/412,618
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid
US-10-395-894-8

Query Match      28.9%; Score 151.4; DB 12; Length 6082;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60
Db 81 CTGCTCCCTGCTGTGTGGAGGTCGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 140

Qy 61 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGC 120
Db 141 ACAAGGCAAGGCTTGACCGACAAATTCATGAAGAATCTGCTTAGGGTTAGCGTTTGGC 200

Qy 121 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 153
Db 201 CTGCTTCGGGATGTACGGGCCAGATATTCGGT 233

RESULT 68
US-10-395-894-9
; Sequence 9, Application US/10395894
; Publication No. US20040033229A1
; GENERAL INFORMATION:
; APPLICANT: MADDON, Paul J.
; APPLICANT: DONOVAN, Gerald P.
; APPLICANT: OLSON, William C.
; APPLICANT: SCHLKE, No. US20040033229A1bert
; APPLICANT: GARDNER, Jason
; APPLICANT: MA, Dangshe
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
; FILE REFERENCE: P00741.70005.US
; CURRENT APPLICATION NUMBER: US/10/395,894
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: PCI/US02/33944
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/335,215
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/362,747
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/412,618
```

```
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 9
/ LENGTH: 6082
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-9

Query Match      28.9%; Score 151.4; DB 12; Length 6082;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB      81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY      61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB      141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200

QY      121 CTGCTTCGGGATGTACGGGCCAGATATTCGGGT 153
DB      201 CTGCTTCGGGATGTACGGGCCAGATATTCGGGT 233

RESULT 69
US-10-395-894-10
/ Sequence 10, Application US/10395894
/ Publication No. US20040033229A1
/ GENERAL INFORMATION:
/ APPLICANT: MADDON, Paul J.
/ APPLICANT: DONOVAN, Gerald P.
/ APPLICANT: OLSON, William C.
/ APPLICANT: SCHLKE, No. US20040033229A1bert
/ APPLICANT: GARDNER, Jason
/ APPLICANT: MA, Dangshe
/ TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
/ FILE REFERENCE: P00741.70005.US
/ CURRENT FILING DATE: 2003-03-24
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 11
/ LENGTH: 6085
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-11

Query Match      28.9%; Score 151.4; DB 12; Length 6085;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB      81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY      61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB      141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200

QY      121 CTGCTTCGGGATGTACGGGCCAGATATTCGGGT 153
DB      201 CTGCTTCGGGATGTACGGGCCAGATATTCGGGT 233

RESULT 71
US-10-395-894-13
/ Sequence 13, Application US/10395894
/ Publication No. US20040033229A1
/ GENERAL INFORMATION:
/ APPLICANT: MADDON, Paul J.
/ APPLICANT: DONOVAN, Gerald P.
/ APPLICANT: OLSON, William C.
/ APPLICANT: SCHLKE, No. US20040033229A1bert
/ APPLICANT: GARDNER, Jason
/ APPLICANT: MA, Dangshe
/ TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
/ FILE REFERENCE: P00741.70005.US
/ CURRENT FILING DATE: 2003-03-24
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 10
/ LENGTH: 6082
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-10

Query Match      28.9%; Score 151.4; DB 12; Length 6082;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB      81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY      61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB      141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200
```

```
QY      121 CTGCTTCGGGATGTACGGGCCAGATATTCGGGT 153
DB      201 CTGCTTCGGGATGTACGGGCCAGATATTCGGGT 233

RESULT 70
US-10-395-894-11
/ Sequence 11, Application US/10395894
/ Publication No. US20040033229A1
/ GENERAL INFORMATION:
/ APPLICANT: MADDON, Paul J.
/ APPLICANT: DONOVAN, Gerald P.
/ APPLICANT: OLSON, William C.
/ APPLICANT: SCHLKE, No. US20040033229A1bert
/ APPLICANT: GARDNER, Jason
/ APPLICANT: MA, Dangshe
/ TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
/ FILE REFERENCE: P00741.70005.US
/ CURRENT FILING DATE: 2003-03-24
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 11
/ LENGTH: 6085
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-11

Query Match      28.9%; Score 151.4; DB 12; Length 6085;
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 60
DB      81 CTGCTCCCTGCTGTGTGTTGGAGTGCCTGAGTAGTGCAGCAAAATTTAAGCTACA 140

QY      61 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 120
DB      141 ACAAGGCAAGGCTTGACCGACAATTCATGAAGAATCTGCTTAGGTTAGCGTTTTCG 200

QY      121 CTGCTTCGGGATGTACGGGCCAGATATTCGGGT 153
DB      201 CTGCTTCGGGATGTACGGGCCAGATATTCGGGT 233

RESULT 71
US-10-395-894-13
/ Sequence 13, Application US/10395894
/ Publication No. US20040033229A1
/ GENERAL INFORMATION:
/ APPLICANT: MADDON, Paul J.
/ APPLICANT: DONOVAN, Gerald P.
/ APPLICANT: OLSON, William C.
/ APPLICANT: SCHLKE, No. US20040033229A1bert
/ APPLICANT: GARDNER, Jason
/ APPLICANT: MA, Dangshe
/ TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
/ FILE REFERENCE: P00741.70005.US
/ CURRENT FILING DATE: 2003-03-24
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR FILING DATE: 2002-09-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 11
/ LENGTH: 6085
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Plasmid
US-10-395-894-11
```

; PRIOR FILING DATE: 2001-10-23  
 ; PRIOR APPLICATION NUMBER: US 60/362,747  
 ; PRIOR FILING DATE: 2002-03-07  
 ; PRIOR APPLICATION NUMBER: US 60/412,618  
 ; PRIOR FILING DATE: 2002-09-20  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 13  
 ; LENGTH: 6094  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Plasmid  
 ; US-10-395-894-13

Query Match 28.9%; Score 151.4; DB 12; Length 6094;  
 Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
 DB 81 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGCTTGACGACAAATTCATGAAGATCTGCTAGGTTAGGCGTTTTCGG 120  
 DB 141 ACAAGGCAAGCTTGACGACAAATTCATGAAGATCTGCTAGGTTAGGCGTTTTCGG 200  
 QY 121 CTGCTTCGCATGTACGGCCAGATATTTCGCGT 153  
 DB 201 CTGCTTCGCATGTACGGCCAGATATTTCGCGT 233

RESULT 72  
 US-10-395-894-12  
 ; Sequence 12, Application US/10395894  
 ; Publication No. US20040033229A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MADDON, Paul J.  
 ; APPLICANT: DONOVAN, Gerald P.  
 ; APPLICANT: OLSON, William C.  
 ; APPLICANT: SCHLKE, No. US28040033229A1bert  
 ; APPLICANT: GARDNER, Jason  
 ; APPLICANT: MA, Dangshe  
 ; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
 ; FILE REFERENCE: P00741.70005.US  
 ; CURRENT APPLICATION NUMBER: US/10/395,894  
 ; CURRENT FILING DATE: 2003-03-24  
 ; PRIOR APPLICATION NUMBER: PCT/US02/33944  
 ; PRIOR FILING DATE: 2002-10-23  
 ; PRIOR APPLICATION NUMBER: US 60/335,215  
 ; PRIOR FILING DATE: 2001-10-23  
 ; PRIOR APPLICATION NUMBER: US 60/362,747  
 ; PRIOR FILING DATE: 2002-03-07  
 ; PRIOR APPLICATION NUMBER: US 60/412,618  
 ; PRIOR FILING DATE: 2002-09-20  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 12  
 ; LENGTH: 6097  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Plasmid  
 ; US-10-395-894-12

Query Match 28.9%; Score 151.4; DB 12; Length 6097;  
 Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
 DB 81 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 140

QY 61 ACAAGGCAAGCTTGACGACAAATTCATGAAGATCTGCTAGGTTAGGCGTTTTCGG 120  
 DB 141 ACAAGGCAAGCTTGACGACAAATTCATGAAGATCTGCTAGGTTAGGCGTTTTCGG 200  
 QY 121 CTGCTTCGCATGTACGGCCAGATATTTCGCGT 153  
 DB 201 CTGCTTCGCATGTACGGCCAGATATTTCGCGT 233

RESULT 73  
 US-09-884-211A-5  
 ; Sequence 5, Application US/09884211A  
 ; Publication No. US20030032791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alan et. al.  
 ; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
 ; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
 ; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
 ; FILE REFERENCE: PCI0743A  
 ; CURRENT APPLICATION NUMBER: US/09/884,211A  
 ; CURRENT FILING DATE: 2000-06-26  
 ; PRIOR APPLICATION NUMBER: 60/213,909  
 ; PRIOR FILING DATE: 2000-06-26  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 6148  
 ; TYPE: DNA  
 ; ORGANISM: pcDNA3.1zeo/murine G-alpha 15  
 ; US-09-884-211A-5

Query Match 28.9%; Score 151.4; DB 10; Length 6148;  
 Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 60  
 DB 81 CTGCTCCCTGCTGTGTGGAGTGTGCTGAGTGTGCGGAGCAAAATTTAAGCTACA 140  
 QY 61 ACAAGGCAAGCTTGACGACAAATTCATGAAGATCTGCTAGGTTAGGCGTTTTCGG 120  
 DB 141 ACAAGGCAAGCTTGACGACAAATTCATGAAGATCTGCTAGGTTAGGCGTTTTCGG 200  
 QY 121 CTGCTTCGCATGTACGGCCAGATATTTCGCGT 153  
 DB 201 CTGCTTCGCATGTACGGCCAGATATTTCGCGT 233

RESULT 74  
 US-09-884-211A-6  
 ; Sequence 6, Application US/09884211A  
 ; Publication No. US20030032791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alan et. al.  
 ; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
 ; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
 ; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
 ; FILE REFERENCE: PCI0743A  
 ; CURRENT APPLICATION NUMBER: US/09/884,211A  
 ; CURRENT FILING DATE: 2000-06-26  
 ; PRIOR APPLICATION NUMBER: 60/213,909  
 ; PRIOR FILING DATE: 2000-06-26  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 6149  
 ; TYPE: DNA  
 ; ORGANISM: pcDNA3.1zeo/human G-alpha 16  
 ; US-09-884-211A-6

Query Match 28.9%; Score 151.4; DB 10; Length 6149;  
 Best Local Similarity 99.3%; Pred. No. 5.2e-41;  
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

RESULT 75
US-09-780-933-5
; Sequence 5, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMEYE HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6186
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1225)..(1572)
US-09-780-933-5

Query Match 28.9%; Score 151.4; DB 9
Best Local Similarity 99.3%; Pred. No. 5.2e-41;
Matches 152; Conservative 0; Mismatches 1

QY 1 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGG
Db 81 CTGCTCCCTGCTGTGTGTGGAGTGCCTGAGTAGTGG
QY 61 ACAAGGCAAGCTTGCACCGACAATTGCATGAAGAATCTC
Db 141 ACAAGGCAAGCTTGCACCGACAATTGCATGAAGAATCTC
QY 121 CTGCTTCGCATGTATCGGGCGAGATATTCGGT 153
Db 201 CTGCTTCGCATGTATCGGGCGAGATATTCGGT 233

```

Search completed: March 11, 2004, 11:20:19  
Job time : 386.636 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 07:44:02 ; Search time 3117.7 Seconds  
(without alignments)  
5009.444 Million cell updates/sec

Title: US-09-733-368A-1\_COPY\_90\_612

Perfect score: 523

Sequence: 1 ctgctccctgattgtgtt.....accacattggtgcaccc 523

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST.\*

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estm.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_htc.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_htc.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfum.\*
- 16: em\_estom.\*
- 17: em\_gss\_hum.\*
- 18: em\_gss\_inv.\*
- 19: em\_gss\_pin.\*
- 20: em\_gss\_vrt.\*
- 21: em\_gss\_fun.\*
- 22: em\_gss\_mam.\*
- 23: em\_gss\_mus.\*
- 24: em\_gss\_pro.\*
- 25: em\_gss\_rod.\*
- 26: em\_gss\_phg.\*
- 27: em\_gss\_vri.\*
- 28: gb\_gss1.\*
- 29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	517.8	99.0	602	28	B67169 CpG0047A Cp
2	196.8	37.6	865	14	CF251529 hdm001_c0
3	151	28.9	863	14	CF251728 hdm003_e1
4	103.8	13.8	377	12	B1065864 pgfln.pk0

5	103.8	19.8	414	14	CF250631
6	103.8	19.8	454	14	CF250926
7	103.8	19.8	648	13	BUI23326
8	103.8	19.8	661	13	BUI338428
9	103.8	19.8	668	13	BUI452326
10	103.8	19.8	673	13	BUI04175
11	103.8	19.8	728	13	BUI17201
12	103.8	19.8	741	13	BUI25810
13	103.8	19.8	777	13	BUI470589
14	103.8	19.8	784	13	BUI44255
15	103.8	19.8	793	13	BUI12414
16	103.8	19.8	801	13	BUI07637
17	103.8	19.8	834	13	BUI14728
18	103.8	19.8	835	13	BUI13305
19	103.8	19.8	859	13	BUI354615
20	103	19.7	725	13	BUI490656
21	102.2	19.5	773	13	BUI32452
22	100.6	19.2	732	13	BUI343905
23	100.6	19.2	744	13	BUI309030
24	100.6	19.2	1012	13	BUI43329
25	95	18.2	695	13	BUI430989
26	93.6	17.9	270	14	CB016682
27	93.4	17.9	669	13	BUI263560
28	92.8	17.7	810	13	BUI356927
29	88.2	16.9	623	13	BUI492375
30	88	16.8	418	13	BUI404431
31	88	16.8	598	13	BUI490064
32	88	16.8	773	13	BUI487895
33	87.8	16.8	801	13	BUI474299
34	86.4	16.5	282	13	BUI415406
35	86.4	16.5	766	13	BUI471721
36	86.4	16.5	780	13	BUI243776
37	84.8	16.2	269	13	BUI43048
38	80.2	15.3	863	13	BUI340356
39	76	14.5	516	13	BUI201513
40	74.8	14.3	611	13	BUI491086
41	73.8	14.1	647	13	BUI491487
42	72.4	13.8	774	13	BUI232252
43	71	13.6	829	13	BUI416333
44	70.4	13.5	773	13	BUI315394
45	70	13.4	642	13	BUI490009
46	69.8	13.3	848	13	BUI350008
47	69.2	13.2	851	13	BUI403961
48	68.2	13.0	647	9	AI981988
49	66.6	12.7	630	13	BUI402803
50	65.4	12.5	619	13	BUI416401
51	63.6	12.2	376	13	BUI452625
52	63.2	12.1	195	13	BQ839774
53	63.2	12.1	195	13	BQ839776
54	63.2	12.1	195	13	BQ839779
55	62.8	12.0	844	13	BUI41765
56	62	11.9	197	13	BQ839752
57	60	11.5	196	13	BQ839750
58	56.6	10.8	751	13	BQ8314089
59	55.8	10.6	945	13	BUI124247
60	55.6	10.6	576	13	BUI406314
61	55.2	10.6	622	13	BUI470895
62	54.6	10.4	750	13	BUI244389
63	53.2	10.2	747	13	BUI413106
64	51.8	9.9	767	13	BUI414993
65	47.2	9.0	725	14	CF252511
66	46.8	8.9	718	13	BUI490848
67	46.6	8.9	724	13	BUI414295
68	45.4	8.7	401	9	AB083460
69	43.4	8.3	575	13	BUI466407
70	43.4	8.3	581	12	BG711671
71	43.4	8.3	608	13	BUI258368
72	43.4	8.3	612	14	CD764079
73	43.4	8.3	662	13	BUI412768
74	43.4	8.3	684	13	BUI238874
75	43.4	8.3	704	13	BUI476993
76	43.4	8.3	708	13	BUI38351
77	43.4	8.3	781	13	BUI361582



78 43.4 8.3 904 13 BU135477  
79 43.4 8.3 933 13 BU123851  
80 43.4 8.3 1024 13 BU128788  
81 43.4 8.3 1197 28 CC272040  
82 43.2 8.3 675 13 BU383902  
83 42.6 8.1 605 12 BU390532  
84 41.8 8.0 625 13 BU265554  
85 41.8 8.0 821 13 BU458548  
86 41.8 8.0 1125 28 CC254909  
87 41.2 7.9 676 13 BU247819  
88 41.2 7.9 798 13 BU388758  
89 40.8 7.6 668 13 BU245786  
90 40.8 7.6 726 13 BU260757  
91 40.4 7.7 783 13 BU307719  
92 40.2 7.7 625 14 CD217797  
93 40 7.6 885 13 BX425603  
94 39.8 7.6 577 29 CE028982  
95 39.8 7.6 1134 28 CC246137  
96 39.2 7.5 708 13 BU334817  
97 39.2 7.5 799 13 BU266652  
98 38.6 7.4 635 13 BU393824  
99 38.2 7.3 1095 28 CC215884  
100 38 7.3 536 13 BU486638

# ALIGNMENTS

RESULT 1  
B67169  
LOCUS Cp60047A Op10WAGDNA2 602 bp DNA linear GSS 12-MAY-2000  
DEFINITION Cryptosporidium parvum genomic, genomic survey sequence.  
ACCESSION B67169  
VERSION B67169.1 GI:2642750  
KEYWORDS GSS,  
SOURCE Cryptosporidium parvum  
ORGANISM Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.  
1 (bases 1 to 602)  
Strong, W.B. and Nelson, R.G.  
Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis  
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)  
20184851  
10717299  
Contact: Nelson, R. G.  
Depts. of Medicine & Pharmaceutical Chemistry  
San Francisco General Hospital-University of California, San Francisco  
Box 0811, San Francisco, CA 94143-0811, USA  
Tel: 415 206 8846  
Fax: 415 206 3353  
Email: malaria@itsa.ucsf.edu  
Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalculated bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.  
Seq primer: T7  
Class: shotgun  
High quality sequence stop: 602.  
Location/Qualifiers  
1. .602  
/organism="Cryptosporidium parvum"  
/mol\_type="genomic DNA"  
/strain="IOWA"  
/db\_xref="taxon:5807"  
/lab\_host="E. coli XL2 Blue MRF"  
/clone\_lib="Cp10WAGDNA2"  
/note="Vector: pCR-Script Amp SK+; Site 1: SrfI; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution

between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center  
(http://sequence-www.stanford.edu/group/techdev/shear.htm)  
. The randomly sheared gDNA was chromatographed on Sephacryl S-400 to remove any small fragments and DNA eluting in the void volume was blunt-ended with T4 DNA Polymerase, treated with alkaline phosphatase to prevent the ligation of multiple fragments, ligated to SrfI I-digested pCR-Script Amp (SK+) vector and transformed into E. coli strain XL10 Gold. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."

## ORIGIN

Query Match 99.0%; Score 517.8; DB 28; Length 602;  
Best Local Similarity 99.6%; Pred. No. 4.3e-151;  
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CTGCTCCCTCTGTGTGTTCGAGGTGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 60  
Db 41 CTGCTCCCTCTGTGTGTTCGAGGTGCTGAGTAGTCGCGAGCAAAATTTAAGCTACA 100  
QY 61 ACAAGGCAAGGCTTACCGCAATTCGATGAAGATCTGCTAGGCTTAGGCGTTTGGC 120  
Db 101 ACAAGGCAAGGCTTACCGCAATTCGATGAAGATCTGCTAGGCTTAGGCGTTTGGC 160  
QY 121 CTGCTCCGATGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 180  
Db 161 CTGCTTCGAGTGTACGGGCCAGATATTCGCTATCTGAGGGGACTAGGCTGTGTTAGG 220  
QY 181 CGAAAGCGGGGCTTCGTTTACGCGGTTAGAGTCCCTCAGGATATAGTAGTTTCG 240  
Db 221 CGAAAGCGGGGCTTCGTTTACGCGGTTAGAGTCCCTCAGGATATAGTAGTTTCG 280  
QY 241 TTTTGCATAGGGGGGGAATAGTCTTATGCACTCTTGTAGTCTGCACATGG 300  
Db 281 TTTTGCATAGGGGGGGAATAGTCTTATGCACTCTTGTAGTCTGCACATGG 340  
QY 301 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAACACCGTCATGCCGATGG 360  
Db 341 TAACGATGAGTTAGCAACATGCCCTTACAGGAGAGAAACACCGTCATGCCGATGG 400  
QY 361 TGGAGTAGAGTGTGATGATCGCTTATTAGGAGGCAACAGACGGTCTGACATGGA 420  
Db 401 TGGAGTAGAGTGTGATGATCGCTTATTAGGAGGCAACAGACGGTCTGACATGGA 460  
QY 421 TTGAGCAACCACTAAATTCGCAATTCGAGATATGTTATTAAGTCTAGCTCGATA 480  
Db 461 TTGAGCAACCACTAAATTCGCAATTCGAGATATGTTATTAAGTCTAGCTCGATA 520  
QY 481 CAATAAACGCCATTTGACCAATTCACCAATTCGTTGTCACC 521  
Db 521 CAATAAACGCCATTTGACCAATTCACCAATTCGTTGTCACC 561

RESULT 2  
CF251529  
LOCUS hdm001\_c06 lPS-activated macrophage cell line Gallus gallus cdna, mRNA sequence.  
DEFINITION CF251529  
ACCESSION CF251529  
VERSION CF251529.1 GI:33484784  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
REFERENCE 1 (bases 1 to 865)  
AUTHORS Wittzell, H., Bed'Hom, B., Morin, V., Young, J.R., Whittaker, C.J., Chausse, A.M. and Zocrob, R.  
TITLE A collection of chicken ESTs from activated immune cells  
JOURNAL Unpublished (2003)

## COMMENT

Contact: Zoorob R  
UPR 1983  
CNRS

7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
Tel: 33 1 49 58 35 00  
Fax: 33 1 49 58 33 81  
Email: zoorob@vif.cnrs.fr.

## FEATURES

Location/Qualifiers

source

1..865  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/cell\_line="HD11"  
/clone\_lib="LPS-activated macrophage cell line"  
/note="Vector: pTriplex2"

## ORIGIN

Query Match 37.6%; Score 196.8; DB 14; Length 865;  
Best Local Similarity 82.7%; Pred. No. 2.5e-50;  
Matches 243; Conservative 0; Mismatches 37; Indels 14; Gaps 1;

QY 229 TAGTATGTTTCGCTTTTCATAGAGGGGGAATAGTCTTATGCAATATCTTCTAGT 288

Db 27 TAGAAGTACGCTTTTCATAGAGGGGGAATAGTCTTATGCAATATCTTCTAGT 83

QY 289 CTTCGCAACATGTTAGCAATGTTAGCAATGCTTACAGGAGAGAGAAACACCGTG 348

Db 84 -----GTAAACGATGAACACAGCAATACGCTTATAGGAGAGAGAGGTTACCGTG 132

QY 349 CATGCCGATGTTGGAGTAAGTGTGTACGATGTCGCTTATTAGGAGGACACAGCGG 408

Db 133 CATGATGTTGGTGGAGTAAGTGTGTACGATGTCGCTTATTAGGAGGTAACAGCGG 192

QY 409 GTCTGACATGATTGGACGACCACTAAATTCGCGATTGCGAGATATTGTATTAAAGTG 468

Db 193 GTCTTACACGATTTGGACGATCTCTTGTATTCGCGATAGTAAGATGTTGTTTAAAGTA 252

QY 469 CTTAGCTCGATACATTAACGCGATTTCACCATTCACCATGTTGTGCACT 522

Db 253 GCTAGCTGTATACAAATAAAGCGCATTTTACCATTCCACCATGTTGTGCACT 306

## RESULT 3

CF251728

LOCUS

DEFINITION hm003\_e10 LPS-activated macrophage cell line Gallus gallus cDNA, mRNA sequence.

ACCESSION

CF251728

VERSION

CF251728.1

KEYWORDS

EST.

SOURCE

ORGANISM

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

Witzell, H., Bed'Hom, B., Morin, V., Young, J.R., Whittaker, C.J.,

Chausse, A.W., and Zoorob, R.

A collection of chicken ESTs from activated immune cells

Unpublished (2003)

Contact: Zoorob R

UPR 1983

CNRS

7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France

Tel: 33 1 49 58 35 00

Fax: 33 1 49 58 33 81

Email: zoorob@vif.cnrs.fr.

Location/Qualifiers

1..863

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/cell\_line="HD11"

## FEATURES

source

1..863

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/cell\_line="HD11"

## ORIGIN

Query Match 28.9%; Score 151; DB 14; Length 863;  
Best Local Similarity 81.0%; Pred. No. 5.9e-36;  
Matches 218; Conservative 0; Mismatches 35; Indels 16; Gaps 3;

QY 229 TAGTATGTTTCGCTTTTCATAGAGGGGGAATAGTCTTATGCAATATCTTCTAGT 288

Db 611 TATGAATAGCGCTTTTCATAGAGGGGGAATAGTCTTATGCAATATCTTCTAGT 667

QY 289 CTTCGCAACATGTTAGCAATGTTAGCAATGCTTACAGGAGAGAGAAACACCGTG 348

Db 668 -----GTAAACGATGAACACGATATGCTTATAGGAGAG-AGGTTACCGTG 715

QY 349 CATGCCGATGTTGGAGTAAGTGTGTACGATGTCGCTTATTAGGAGGCAACAGACGG 408

Db 716 CATGATGATTGGTGAAGTAAGTGTGTACGATGTCGCTTATTAGGAGGTAACAGACGG 775

QY 409 GTCTGACATGATTGGACGACCACTAAATTCGCGATTGCGAGATATTGTATTAAAGTG 468

Db 776 GTCTTACACGATTTGGACGATCTCTTGTATTCGCGATAGTA-ATGTTGTTTAAAGTA 834

QY 469 CTTAGCTCGATACATTAACGCGCATTTGA 497

Db 835 GCTAGCTTGATACATAAAGCGCATTTTA 863

## RESULT 4

Bi065864

LOCUS

DEFINITION

pgfin.pk006.c7 normalized chicken fat cDNA library Gallus gallus

cDNA clone pgfin.pk006.c7 5' similar to emb|X54094.1|GGF1L Gallus

gallus endogenous virus-21 JF1L-1 DNA sequence, mRNA sequence.

ACCESSION

Bi065864

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 377)

Cogburn, L.A., Morgan, R.W. and Burnside, J.

Chicken ESTs from fat

Unpublished (2001)

CONTACT: Larry A. Cogburn

University of Delaware

Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-1335

Fax: 302-831-2822

Email: cogburn@udel.edu, www.chickest.udel.edu.

Location/Qualifiers

1..377

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/clone="pgfin.pk006.c7"

/sex="Male and Female"

/tissue\_type="fat"

/lab\_host="E.coli EMDH10B"

/clone\_lib="normalized chicken fat cDNA library"

/note="Vector: pSPORT1"

## ORIGIN

Query Match 19.8%; Score 103.8; DB 12; Length 377;  
Best Local Similarity 90.2%; Pred. No. 2.7e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCCTATCTGAGGGACCTAGGTTGTTTATAGCGAGAAAGCGGGCTTCGGTTGTACGCGT 209

Db 76 GCTTACTGAGGGGACCTAGTATGTTATAGCGAGAAAGCGGGCTTCGGTTGTACGCGT 135

Qy 210 TAGGAGTCCCTCAGCATATAGTATTCGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
 |||||  
 Db 136 TAGAGTCCCTCAGCATATAGTATTCGCTTTTGCATAGGAGGGGGAATGTAGTCA 195  
 |||||  
 Qy 270 TAT 272  
 ||  
 Db 196 AAT 198

RESULT 5  
 CF250631  
 LOCUS es015 c01 Eimeiria tenella-infected caecal tonsil Gallus gallus EST 07-AUG-2003  
 DEFINITION cDNA, mRNA sequence.  
 ACCESSION CF250631.1 GI:33483886  
 VERSION CF250631  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 414).  
 AUTHORS Wittzell,H., Bed'Hom,B., Morin,V., Young,J.R., Whittaker,C.J.,  
 Chausse,A.M. and Zoorob,R.  
 TITLE A collection of chicken ESTs from activated immune cells  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Zoorob R  
 UPR 1983

CNRS  
 7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
 Tel: 33 1 49 58 35 00  
 Fax: 33 1 49 58 33 81  
 Email: zoorob@vjf.cnrs.fr.  
 Location/Qualifiers  
 source  
 1. .414  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone\_lib="Eimeiria tenella-infected caecal tonsil"  
 /note="Organ: Caecal tonsil; Vector: pTriplex2"

Query Match 19.8%; Score 103.8; DB 14; Length 414;  
 Best local Similarity 90.2%; Pred. No. 2.8e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGGCGGAAAGCGGGCTTCGGTTGTACGGGT 209  
 |||||  
 Db 113 GCTTGACTGAGGGGACCATAGTATGTATAGGCGAAGCGGGCTTCGGTTGTACGGGT 172  
 |||||  
 Qy 210 TAGGAGTCCCTCAGCATATAGTATTCGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
 |||||  
 Db 173 TAGGAGTCCCTCAGCATATAGTATTCGCTTTTGCATAGGAGGGGGAATGTAGTCA 232  
 |||||  
 Qy 270 TAT 272  
 ||  
 Db 233 AAT 235

RESULT 6  
 CF250926  
 LOCUS es018 g07 Eimeiria tenella-infected caecal tonsil Gallus gallus EST 07-AUG-2003  
 DEFINITION cDNA, mRNA sequence.  
 ACCESSION CF250926  
 VERSION CF250926.1 GI:33484181  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 454).  
 AUTHORS Wittzell,H., Bed'Hom,B., Morin,V., Young,J.R., Whittaker,C.J.,  
 Chausse,A.M. and Zoorob,R.  
 TITLE A collection of chicken ESTs from activated immune cells  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Zoorob R  
 UPR 1983

CNRS  
 7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
 Tel: 33 1 49 58 35 00  
 Fax: 33 1 49 58 33 81  
 Email: zoorob@vjf.cnrs.fr.  
 Location/Qualifiers  
 source  
 1. .454  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone\_lib="Eimeiria tenella-infected caecal tonsil"  
 /note="Organ: Caecal tonsil; Vector: pTriplex2"

Query Match 19.8%; Score 103.8; DB 14; Length 454;  
 Best local Similarity 90.2%; Pred. No. 2.9e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGGCGGAAAGCGGGCTTCGGTTGTACGGGT 209  
 |||||  
 Db 123 GCTTGACTGAGGGGACCATAGTATGTATAGGCGAAGCGGGCTTCGGTTGTACGGGT 182  
 |||||  
 Qy 210 TAGGAGTCCCTCAGCATATAGTATTCGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
 |||||  
 Db 183 TAGGAGTCCCTCAGCATATAGTATTCGCTTTTGCATAGGAGGGGGAATGTAGTCA 242  
 |||||  
 Qy 270 TAT 272  
 ||  
 Db 243 AAT 245

RESULT 7  
 BU123326  
 LOCUS 603147220F1 CSEQCHL18 Gallus gallus cDNA clone CHEST1486 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BU123326  
 VERSION BU123326.1 GI:25333962  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 648)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 source  
 1. .648  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"

/clone="CHESTR149g6"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHL18"  
 /note="Organ: small intestine; Vector: pBluescript II  
 KS(+); Site 1: EcoRI; Site 2: NotI; Modification of  
 pBluescript II KS(+) [Stratagene] vector to accommodate  
 cDNA produced with the T-trimmed protocol (Construction of  
 uni-directionally cloned cDNA libraries from messenger RNA  
 for improved 3' end DNA sequencing by Glenn Fu, et al.  
 U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with  
 NotI and EcoRI. Ligate in double stranded adaptor  
 containing BglI and BamHI sites  
 containing BglI and BamHI sites  
 [5'ggcgctgcagcccgatccgaaagaaag]  
 [5'aattcttttgcgatccgggtgcagc]"

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 648;  
 Best Local Similarity 90.2%; Pred. No. 3.4e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGCGGAAAGCGGGCTTCGGTGTGACGGGT 209  
 |||  
 Db 337 GCTTGACTGAGGGGACCTAGTATGTATAGCGGAAAGCGGGCTTCGGTGTGACGGGT 396  
 |||

QY 210 TAGAGTCCCTCAGCATATAGTATGCTTTGTCATAGGAGGGGGAAATGTAGTCT 269  
 |||  
 Db 397 TAGAGTCCCTCAGCATATAGTATGCTTTGTCATAGGAGGGGGAAATGTAGTCTA 456  
 |||

QY 270 TAT 272  
 |||  
 Db 457 AAT 459

RESULT 8  
 BU338428  
 LOCUS  
 DEFINITION 661 bp mRNA linear EST 28-NOV-2002  
 sequence.  
 ACCESSION BU338428  
 VERSION BU338428.1 GI:25846429  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 661)  
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source  
 1..661  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST448e12"  
 /dev\_stage="16 day embryo"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN66"

/note="Organ: brain; Vector: pBluescript II KS(+); Site 1:  
 EcoRI; Site 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunt-ended, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 661;  
 Best Local Similarity 90.2%; Pred. No. 3.4e-21;  
 Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGCTGTGTTAGCGGAAAGCGGGCTTCGGTGTGACGGGT 209  
 |||  
 Db 351 GCTTGACTGAGGGGACCTAGTATGTATAGCGGAAAGCGGGCTTCGGTGTGACGGGT 410  
 |||

QY 210 TAGAGTCCCTCAGCATATAGTATGCTTTGTCATAGGAGGGGGAAATGTAGTCT 269  
 |||  
 Db 411 TAGAGTCCCTCAGCATATAGTATGCTTTGTCATAGGAGGGGGAAATGTAGTCTA 470  
 |||

QY 270 TAT 272  
 |||  
 Db 471 AAT 473

RESULT 9  
 BU452326  
 LOCUS  
 DEFINITION 668 bp mRNA linear EST 29-NOV-2002  
 sequence.  
 ACCESSION BU452326  
 VERSION BU452326.1 GI:25941637  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 668)  
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source  
 1..668  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer"  
 /db\_xref="taxon:9031"  
 /clone="CHEST698124"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN14"  
 /note="Organ: ovary; Vector: pBluescript II KS(+); Site 1:

EcORI, Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcORI, size-selected, and cloned into the NotI and EcORI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 668;  
Best Local Similarity 90.2%; Pred. No. 3.4e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGTGTGTTTATAGGCGGAAAGCGGGGCTTCGGTTGTACGGGT 209  
|||  
Db 360 GGTGACTGAGGGGACCATAGTATGTATAGGCGGAAAGCGGGGCTTCGGTTGTACGGGT 419  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTGCTATAGGAGGGGGAATGTAGTCT 269  
|||  
Db 420 TAGGAGTCCCTCAGGATATAGTATGCTTTGCTATAGGAGGGGGAATGTAGTCTA 479  
|||

QY 270 TAT 272  
|||  
Db 480 AAT 482

RESULT 10  
BU104175  
LOCUS 603004302F1 CSQCHL01 Gallus gallus cDNA clone CHEST19d2 5', mRNA  
DEFINITION  
ACCESSION  
VERSION BU104175.1 GI:25305018  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 673)  
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..673  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST19d2"  
/tissue\_type="whole embryo"  
/dev\_stage="20-21"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHL01"  
/note="Organ: whole embryo; Vector: pBluescript II KS(+); Site\_1: EcORI; Site\_2: NotI; Modification of pBluescript

II KS(+). [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcORI. Ligate in double stranded adaptor containing BspI and BamHI sites  
[5'ggcgcgtgcagcccgatccgaaaaag]  
[5'aattcttttttcggatccggggtgcagc]"

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 673;  
Best Local Similarity 90.2%; Pred. No. 3.5e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGTGTGTTTATAGGCGGAAAGCGGGGCTTCGGTTGTACGGGT 209  
|||  
Db 344 GTTGTGCTGAGGGGACCATAGTATGTATAGGCGGAAAGCGGGGCTTCGGTTGTACGGGT 403  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTGCTATAGGAGGGGGAATGTAGTCT 269  
|||  
Db 404 TAGGAGTCCCTCAGGATATAGTATGCTTTGCTATAGGAGGGGGAATGTAGTCTA 463  
|||

QY 270 TAT 272  
|||  
Db 464 AAT 466

RESULT 11  
BU417201  
LOCUS 603671572F1 CSQREL07 Gallus gallus cDNA clone CHEST616p18 5', mRNA  
DEFINITION  
ACCESSION  
VERSION BU417201  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 728)  
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..728  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST616p18"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQREL07"  
/note="Organ: pancreas; Vector: pBluescript II KS(+); Site\_1: EcORI; Site\_2: NotI; Modification of pBluescript II KS(+). [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al.

U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BglI and BamHI sites  
[5'ggcgcgtgcagcccgatccgaaaaag]  
[5'aattcttttttcggatccgggctgcagc]

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 728;  
Best Local Similarity 90.2%; Pred. No. 3.6e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTTAGCGGAAAGCGGGGCTTCGGTTTACGCGGT 209  
|||  
Db 523 GCTTGACTGAGGGGACCATAGTATGTATAGCGAAAGCGGGGCTTCGGTTTACGCGGT 582  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTATGTTTCGCTTTTGCATAGGAGGGGAAATGATGCT 269  
|||  
Db 583 TAGGAGTCCCTCAGGATATAGTATGCGCTTTTGCATAGGAGGGGAAATGATGCTCA 642  
|||

QY 270 TAT 272  
|||  
Db 643 AAT 645

## RESULT 12

BU325810  
LOCUS 741 bp mRNA linear EST 28-NOV-2002  
DEFINITION 603489965F1 CSBQCHN63 Gallus gallus cDNA clone CHEST390b18 5', mRNA sequence.  
ACCESSION BU325810  
VERSION BU325810.1 GI:25833811  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 741)  
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers 1. .741  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST390b18"  
/dev\_stage="3c"  
/lab\_host="DH10B"  
/clone\_lib="CSBQCHN63"  
/note="Organ: heads; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS

## FEATURES

## source

1. .741  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST390b18"  
/dev\_stage="3c"  
/lab\_host="DH10B"  
/clone\_lib="CSBQCHN63"  
/note="Organ: heads; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 741;  
Best Local Similarity 90.2%; Pred. No. 3.6e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTTAGCGGAAAGCGGGGCTTCGGTTTACGCGGT 209  
|||  
Db 578 GCTTGACTGAGGGGACCATAGTATGTATAGCGAAAGCGGGGCTTCGGTTTACGCGGT 637  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTATGTTTCGCTTTTGCATAGGAGGGGAAATGATGCT 269  
|||  
Db 638 TAGGAGTCCCTCAGGATATAGTATGCGCTTTTGCATAGGAGGGGAAATGATGCTCA 697  
|||

QY 270 TAT 272  
|||  
Db 698 AAT 700

## RESULT 13

BU470589  
LOCUS 777 bp mRNA linear EST 30-NOV-2002  
DEFINITION 603760251F1 CSBQREN21 Gallus gallus cDNA clone CHEST677f14 5', mRNA sequence.  
ACCESSION BU470589  
VERSION BU470589.1 GI:25964166  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 777)  
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers 1. .777  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer"  
/db\_xref="taxon:9031"  
/clone="CHEST677f14"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSBQREN21"  
/note="Organ: ovary; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS

## FEATURES

## source

1. .777  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer"  
/db\_xref="taxon:9031"  
/clone="CHEST677f14"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSBQREN21"  
/note="Organ: ovary; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

(1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 777;  
Best Local Similarity 90.2%; Pred. No. 3.7e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTAGGCGGACTAGGGTGTGTTTAGCGGAAAGCGGGCTTCGGTTGACGGGT 209  
|||  
DB 558 GCTTGACTAGGCGGACCATAGTATGATAGCGGAGCGGGCTTCGGTTGACGGGT 617  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTCGTTTGCATAGGAGGGGAAATGAGTCT 269  
|||  
DB 618 TAGGAGTCCCTCAGGATATAGTATGCTTCGTTTGCATAGGAGGGGAAATGAGTCA 677  
|||

QY 270 TAT 272  
|||  
DB 678 AAT 680

## RESULT 14

BU444255  
LOCUS BU444255 784 bp mRNA linear EST 29-NOV-2002  
DEFINITION 603767471F1 CSEQBN13 Gallus gallus cDNA clone CHEST695n18 5', mRNA  
sequence.  
ACCESSION BU444255  
VERSION BU444255.1 GI:25933566  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 784)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source  
1. .784  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer"  
/db\_xref="taxon:9031"  
/clone="CHEST695n18"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQBN13"  
/note="Organ: ovary; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer

reannealing hybridization was used."

## ORIGIN

Query Match 19.8%; Score 103.8; DB 13; Length 784;  
Best Local Similarity 90.2%; Pred. No. 3.7e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCGTATCTAGGCGGACTAGGGTGTGTTTAGCGGAAAGCGGGCTTCGGTTGACGGGT 209  
|||  
DB 482 GCTTGACTAGGCGGACCATAGTATGATAGCGGAGCGGGCTTCGGTTGACGGGT 541  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTCGTTTGCATAGGAGGGGAAATGAGTCT 269  
|||  
DB 542 TAGGAGTCCCTCAGGATATAGTATGCTTCGTTTGCATAGGAGGGGAAATGAGTCA 601  
|||

QY 270 TAT 272  
|||  
DB 602 AAT 604

## RESULT 15

BU312414  
LOCUS BU312414 793 bp mRNA linear EST 28-NOV-2002  
DEFINITION 603841447F1 CSEQCHN61 Gallus gallus cDNA clone CHEST51ml2 5', mRNA  
sequence.  
ACCESSION BU312414  
VERSION BU312414.1 GI:25820415  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source  
1. .793  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST51ml2"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN61"  
/note="Organ: heart; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom Modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

Query Match 19.8%; Score 103.8; DB 13; Length 834;  
Best Local Similarity 90.2%; Pred.No. 3.8e-21;  
Matches 111; Conservative 0; Mismatches 12; Indels 0;

150 GCGTATCTGAGGGGACTAGGCTGTGTTTAGCGGAAAGCGGGGCTTCGGTTGTACGCGGT 209



```

Db      529 GCTTGACTAGGGGACCATAGTATGTATAGCGGAAAGCGGGCTTCGGTTGTACGCGT 588
QY      210 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCT 269
Db      589 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCA 648
QY      270 TAT 272
Db      649 AAT 651

RESULT 18
LOCUS   BU413305
DEFINITION BU413305.1 835 bp mRNA linear EST 29-NOV-2002
          603155306F1 CSEQRL05 Gallus gallus cDNA clone CHEST16812 5', mRNA
          sequence.
ACCESSION BU413305
VERSION   BU413305.1 GI:25905976
KEYWORDS EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
          Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 835)
AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
          Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE     A Comprehensive Collection of Chicken cDNAs
JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE   22335534
PubMed    12445392
COMMENT   Contact: Simon Hubbard
          Department of Biomolecular Sciences
          University of Manchester Institute of Science and Technology
          (UMIST)
          PO Box 88, Manchester, M60 1QD, UK
          Tel: 01612008930
          Fax: 01612360409
          Email: Simon.Hubbard@umist.ac.uk.

FEATURES
         source
         1..835
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /strain="layer"
            /db_xref="taxon:9031"
            /clone="CHEST16812"
            /sex="Female"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="CSEQRL05"
            /notes="Organ: ovary; Vector: pBluescript II KS(+); Site 1:
            EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
            (Stratagene) vector to accommodate cDNA produced with the
            T-trimmed protocol (Construction of uni-directionally
            cloned cDNA libraries from messenger RNA for improved 3'
            end DNA sequencing by Glenn Fu, et al. U.S. Patent #
            6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
            Ligate in double stranded adaptor containing BspI and
            BamHI sites [5'ggccgctgcagccggatccgaaaaaag]
            [5'aattcttttttcggatccggggtgcagc]"

ORIGIN
Query Match 19.8%; Score 103.8; DB 13; Length 835;
Best Local Similarity 90.2%; Pred. No. 3.8e-21;
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      150 GCGTATCTGAGGGGACTAGGCTGCTTTAGCGGAAAGCGGGCTTCGGTTGTACGCGT 209
Db      532 GCTTGACTAGGGGACCATAGTATGTATAGCGGAAAGCGGGCTTCGGTTGTACGCGT 591
QY      210 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCT 269

```

```

Db      592 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCA 651
QY      270 TAT 272
Db      652 AAT 654

RESULT 19
LOCUS   BU354615
DEFINITION BU354615.1 859 bp mRNA linear EST 28-NOV-2002
          603473642F1 CSEQCHN70 Gallus gallus cDNA clone CHEST353d11 5', mRNA
          sequence.
ACCESSION BU354615
VERSION   BU354615.1 GI:25862616
KEYWORDS EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
          Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 859)
AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
          Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE     A Comprehensive Collection of Chicken cDNAs
JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE   22335534
PubMed    12445392
COMMENT   Contact: Simon Hubbard
          Department of Biomolecular Sciences
          University of Manchester Institute of Science and Technology
          (UMIST)
          PO Box 88, Manchester, M60 1QD, UK
          Tel: 01612008930
          Fax: 01612360409
          Email: Simon.Hubbard@umist.ac.uk.

FEATURES
         source
         1..859
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /strain="White Leghorn, HiseX"
            /db_xref="taxon:9031"
            /clone="CHEST353d11"
            /dev_stage="36"
            /lab_host="DH10B"
            /clone_lib="CSEQCHN70"
            /notes="Organ: hearts; Vector: pBluescript II KS(+);
            Site 1: EcoRI; Site 2: NotI; This normalized library was
            constructed from 1 million independent clones. cDNA
            synthesis was initiated using an oligo(dT) primer, using
            methylated C in the first strand synthesis reaction.
            Following this first strand reaction, double-stranded cDNA
            was blunted, ligated to NotI adapters, digested with
            EcoRI, size-selected, and cloned into the NotI and EcoRI
            compatible sites of a custom modified MCS of the
            pBluescript (KS+) vector. The library was normalized in 2
            rounds using conditions adapted from Soares et al., PNAS
            (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
            (1996): 791, except that a significantly longer
            reannealing hybridization was used."

ORIGIN
Query Match 19.8%; Score 103.8; DB 13; Length 859;
Best Local Similarity 90.2%; Pred. No. 3.8e-21;
Matches 111; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      150 GCGTATCTGAGGGGACTAGGCTGCTTTAGCGGAAAGCGGGCTTCGGTTGTACGCGT 209
Db      549 GCTTGACTAGGGGACCATAGTATGTATAGCGGAAAGCGGGCTTCGGTTGTACGCGT 608
QY      210 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCT 269
Db      609 TAGGAGTCCCTCAGGATATAGTATGCTTCGCTTTTCATAGGAGGGGGAATGTAGTCA 668

```

QY 270 TAT 272  
 Db 569 ANT 671  
 RESULT 20  
 BU490656 725 bp mRNA linear EST 30-NOV-2002  
 LOCUS 604129304F1 CSEQBN37 Gallus gallus cDNA clone CHEST953h2 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BU490656  
 VERSION BU490656.1 GI:25984233  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 725)  
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..725  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHEST953h2"  
 /sex="Male and female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQBN37"  
 /note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI. This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used."

Query Match 19.7%; Score 103; DB 13; Length 725;  
 Best Local Similarity 91.6%; Pred. No. 6.3e-21;  
 Matches 109; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCCTACTGAGGGGACTAGGCTGTGTTAGCGAAGAGCGGGCTTCGGTTGTACGCGGT 209  
 Db 558 CTTTGACTGAGGGACCATAGTATGATAGGCGAAGCGGGCTTCGGTTGTACGCGGT 617  
 QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 268  
 Db 618 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 676

## ORIGIN

RESULT 21  
 BUI32452 773 bp mRNA linear EST 25-NOV-2002  
 LOCUS 603120761F1 CSEQCHL22 Gallus gallus cDNA clone CHEST82i15 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BUI32452  
 VERSION BUI32452.1 GI:25344537  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 773)  
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..773  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST82i15"  
 /dev\_stage="36"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHL22"  
 /note="Organ: heads; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI. Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol. (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BspI and BamHI sites [5'ggccggtgcagccgcggtccgaaaaag] [5'aattcttttttggatccggggtgcagcg]"

## FEATURES

source

## ORIGIN

Query Match 19.5%; Score 102.2; DB 13; Length 773;  
 Best Local Similarity 89.4%; Pred. No. 1.2e-20;  
 Matches 110; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 150 GCCTACTGAGGGGACTAGGCTGTGTTAGCGAAGAGCGGGCTTCGGTTGTACGCGGT 209  
 Db 513 CTTTGACTGAGGGACCATAGTATGATAGGCGAAGCGGGCTTCGGTTGTACGCGGT 572  
 QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTC 269  
 Db 573 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCA 632  
 QY 270 TAT 272  
 Db 633 AAT 635

## RESULT 22

BUI343905 732 bp mRNA linear EST 28-NOV-2002  
 LOCUS 603525493F1 CSEQCHN68 Gallus gallus cDNA clone CHEST471i24 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BUI343905

```

VERSION      BU343905.1  GI:25851906
KEYWORDS     EST.
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
REFERENCE    Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
AUTHORS      Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE        A Comprehensive Collection of Chicken cDNAs
JOURNAL      Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE      22335534
PUBMED       12445392
COMMENT      Contact: Simon Hubbard
              Department of Biomolecular Sciences
              University of Manchester Institute of Science and Technology
              (UMIST)
              PO Box 88, Manchester, M60 1QD, UK
              Tel: 01612008930
              Fax: 01612360409
              Email: Simon.Hubbard@umist.ac.uk.
              Location/Qualifiers
FEATURES     source
             1. .732
                /organism="Gallus gallus"
                /mol_type="mRNA"
                /strain="Compton Line 151"
                /db_xref="taxon:9031"
                /clone="CHST471124"
                /sex="Female"
                /tissue_type="cerebellum"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="CSEQCHM68"
                /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
              EcoRI; Site 2: NotI; This normalized library was
              constructed from 1 million independent clones. cDNA
              synthesis was initiated using an oligo(dT) primer, using
              methylated C in the first strand synthesis reaction.
              Following this first strand reaction, double-stranded cDNA
              was blunted, ligated to NotI adapters, digested with
              EcoRI, size-selected, and cloned into the NotI and EcoRI
              compatible sites of a custom modified MCS of the
              pBluescript (KS+) vector. The library was normalized in 2
              rounds using conditions adapted from Soares et al., PNAS
              (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
              (1996): 791, except that a significantly longer
              reannealing hybridization was used."
ORIGIN
Query Match      19.2%; Score 100.6; DB 13; Length 732;
Best Local Similarity 88.6%; Pred. No. 3.6e-20;
Matches 109; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 150 GCGTATCTGAGGGGACTAGGTGTGTTTAGGCGAAAGCGGGGCTTCGGTGTGACGGGT 209
    |||
Db 425 GCTTGACTGAGGGGACCACTAGTATGATAGGCGGCGGCTTCGGTGTGACGGGT 484
QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTGCGTTTGCATAGGAGGGGGAATGTAGTCT 269
    |||
Db 485 TAGGAGTCCCTCAGGATACAGTATGCTTTGCGTTTGCATAGGAGGGGGAATGTAGTCA 544
QY 270 TAT 272
    |||
Db 545 AAT 547

RESULT 23
BU309030
LOCUS      744 bp  mRNA  linear  EST 28-NOV-2002
DEFINITION 603538660F1 CSEQCHN60 Gallus gallus cDNA clone CHEST504g16 5', mRNA
sequence.
ACCESSION  BU143329
VERSION     BU309030

```

```

VERSION      BU309030.1  GI:25817031
KEYWORDS     EST.
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
REFERENCE    Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
AUTHORS      Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE        A Comprehensive Collection of Chicken cDNAs
JOURNAL      Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE      22335534
PUBMED       12445392
COMMENT      Contact: Simon Hubbard
              Department of Biomolecular Sciences
              University of Manchester Institute of Science and Technology
              (UMIST)
              PO Box 88, Manchester, M60 1QD, UK
              Tel: 01612008930
              Fax: 01612360409
              Email: Simon.Hubbard@umist.ac.uk.
              Location/Qualifiers
FEATURES     source
             1. .744
                /organism="Gallus gallus"
                /mol_type="mRNA"
                /strain="Compton Line 151"
                /db_xref="taxon:9031"
                /clone="CHST504g16"
                /sex="Female"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="CSEQCHM60"
                /note="Organ: heart; Vector: pBluescript II KS(+); Site_1:
              EcoRI; Site 2: NotI; This normalized library was
              constructed from 1 million independent clones. cDNA
              synthesis was initiated using an oligo(dT) primer, using
              methylated C in the first strand synthesis reaction.
              Following this first strand reaction, double-stranded cDNA
              was blunted, ligated to NotI adapters, digested with
              EcoRI, size-selected, and cloned into the NotI and EcoRI
              compatible sites of a custom modified MCS of the
              pBluescript (KS+) vector. The library was normalized in 2
              rounds using conditions adapted from Soares et al., PNAS
              (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
              (1996): 791, except that a significantly longer
              reannealing hybridization was used."
ORIGIN
Query Match      19.2%; Score 100.6; DB 13; Length 744;
Best Local Similarity 88.6%; Pred. No. 3.6e-20;
Matches 109; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 150 GCGTATCTGAGGGGACTAGGTGTGTTTAGGCGAAAGCGGGGCTTCGGTGTGACGGGT 209
    |||
Db 223 GCTTGACTGAGGGGACCACTAGTATGATAGGCGGCGGCTTCGGTGTGACGGGT 282
QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTGCGTTTGCATAGGAGGGGGAATGTAGTCT 269
    |||
Db 283 TAGGAGTCCCTCAGGATACAGTATGCTTTGCGTTTGCATAGGAGGGGGAATGTAGTCA 342
QY 270 TAT 272
    |||
Db 343 AAT 345

RESULT 24
BU143329
LOCUS      1012 bp  mRNA  linear  EST 25-NOV-2002
DEFINITION 603230107F1 CSEQCHL26 Gallus gallus cDNA clone CHEST224m2 5', mRNA
sequence.
ACCESSION  BU143329
VERSION     BU143329.1  GI:25359668

```

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
MEDLINE  
PUBMED

COMMENT

Phasianinae; Gallus.  
1 (bases 1 to 695)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers  
1. .695  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST950el7"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSQRBN37"  
/notes="Organ: pancreas; Vector: pBluescript II KS(+);  
Site 1: EcoRI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunt-ended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

ORIGIN

Query Match 19.2%; Score 100.6; DB 13; Length 1012;  
Best Local Similarity 88.6%; Pred. No. 4.1e-20;  
Matches 109; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGTGTGTTAGGCGAAGAGCGGGCTTCGGTTGTACGGGT 209  
|||  
Db 590 GCTTGACTGAGGGGACCATAGTATGTATAGGCGAAGCGGGCTTCGGTTGTACGGGT 649  
|||  
QY 210 TAGGAGTCCCTCAGGATATAGTATGTTTTCGTTTTCATAGGAGGGGAGAA 260  
|||  
Db 650 TAGGAGTCCCTCAGGATATAGTATGTTTTCGTTTTCATAGGAGTCGGAATGTATGTC 709  
|||

QY 270 TAT 272  
|||  
Db 710 AAT 712

RESULT 25  
BU490989  
LOCUS  
DEFINITION

604127967F1 CSQRBN37 Gallus gallus cDNA clone CHEST950el7 5', mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BU490989 695 bp mRNA linear EST 30-NOV-2002  
604127967F1 CSQRBN37 Gallus gallus cDNA clone CHEST950el7 5', mRNA  
sequence.

BU490989 1 GI:25984566  
EST.  
Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
MEDLINE  
PUBMED

COMMENT

Phasianinae; Gallus.  
1 (bases 1 to 695)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers  
1. .695  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST950el7"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSQRBN37"  
/notes="Organ: pancreas; Vector: pBluescript II KS(+);  
Site 1: EcoRI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunt-ended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

ORIGIN

Query Match 18.2%; Score 95; DB 13; Length 695;  
Best Local Similarity 91.0%; Pred. No. 2e-18;  
Matches 101; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGGACTAGGTGTGTTAGGCGAAGAGCGGGCTTCGGTTGTACGGGT 209  
|||  
Db 581 GCTTGACTGAGGGGACCATAGTATGTATAGGCGAAGCGGGCTTCGGTTGTACGGGT 640  
|||  
QY 210 TAGGAGTCCCTCAGGATATAGTATGTTTTCGTTTTCATAGGAGGGGAGAA 260  
|||  
Db 641 TAGGAGTCCCTCAGGATATAGTATGTTTTCGTTTTCATAGGAGGGGAGAA 691  
|||

RESULT 26  
CB016682  
LOCUS  
DEFINITION

270 bp mRNA linear EST 10-JAN-2003  
pBnic.pk013.d10 Chicken lymphoid cDNA library (pBnic) Gallus gallus  
cDNA clone pBnic.pk013.d10 5' similar to gb|AF013304.1 Avian  
leukosis virus strain av-3, complete genome, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CB016682 1 GI:27591418  
EST.  
Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 270)  
Morgan, R.W. and Burnside, J.  
Chicken ESTs from lymphoid tissue

JOURNAL  
COMMENT

Unpublished (2002)  
Contact: Robin W. Morgan  
University of Delaware  
Townsend Hall, Newark, DE 19717, USA  
Tel: 302-831-1341  
Fax: 302-831-2822  
Email: morgan@udel.edu, www.chickest.udel.edu.  
Location/Qualifiers

## FEATURES

source  
1..270  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="pgnic.pk013.d10"  
/sex="Male and Female"  
/tissue\_type="thymus, bursa, spleen, PBL, bone marrow"  
/lab\_host="E. coli EMDH10B"  
/clone\_lib="Chicken lymphoid cDNA library (pgnic)"  
/note="Vector: pcwvSPORT 6"

## ORIGIN

Query Match 17.9%; Score 93.6; DB 14; Length 270;  
Best Local Similarity 84.7%; Pred. No. 3.8e-18;  
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 150 GCGTATCTAGGGGACTAGGCTGTGTTTAGGCGAAGACGGGGCTTCGGTTGTACGGCGT 209  
Db 120 GCTTGACTGAGGGGACCATAGTATGTATAGGCGAAGACGGGGCTTCGGTTGTACGGCGT 179  
QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCT 269  
Db 180 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGAATGTAGTCT 239  
QY 270 TATG 273  
Db 240 GAGG 243

## RESULT 27

BU263560 669 bp mRNA linear EST 26-NOV-2002  
LOCUS 603014517F1 CSEQCHN52 Gallus gallus cDNA clone CHEST806a6 5', mRNA  
DEFINITION sequence.  
ACCESSION BU263560  
VERSION BU263560.1 GI:25533091  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
REFERENCE 1 (bases 1 to 669)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..669  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST806a6"  
/dev\_stage="22"

/lab\_host="DH10B"  
/clone\_lib="CSEQCHN52"

/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 17.9%; Score 93.4; DB 13; Length 669;  
Best Local Similarity 90.1%; Pred. No. 6.3e-18;  
Matches 100; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 150 GCGTATCTAGGGGACTAGGCTGTGTTTAGGCGAAGACGGGGCTTCGGTTGTACGGCGT 209  
Db 559 GCTTGACTGAGGGGACCATAGTATGTATAGGCGAAGACGGGGCTTCGGTTGTACGGCGT 618  
QY 210 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGA 260  
Db 619 TAGGAGTCCCTCAGGATATAGTATGCTTTTGCATAGGAGGGGGA 669

## RESULT 28

BU356927 810 bp mRNA linear EST 28-NOV-2002  
LOCUS 603475272F1 CSEQCHN70 Gallus gallus cDNA clone CHEST357p17 5', mRNA  
DEFINITION sequence.  
ACCESSION BU356927  
VERSION BU356927.1 GI:25864928  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
REFERENCE 1 (bases 1 to 810)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers

FEATURES  
source

1..810  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST357p17"  
/dev\_stage="36"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN70"  
/note="Organ: hearts; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using

Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the phagescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

	Query Match	16.9%	Score 88.2	DB 13	Length 623
	Best Local Similarity	88.1%	Pred. No. 2.6e-16		
	Matches 96	Conservative 0	Mismatches 13	Indels 0	Gaps 0
QY	150	GGGTATCTGAGGGGACTAGGGTGTCTTTAGCGAAAGCGGGCTTCGGTTGTACGCGGT	209		
Db	509	GTCTTGACTGAGGGGACCATAGTATGTATAGCGAAAGCGGGCTTCGGTTGTACGCGGT	568		
QY	210	TAGAGTCCCTCAGGATATAGTATTCGCTTTTCATAGGAGGGGG	258		
Db	569	TAGAGTCCCTCAGGATATAGTATTCGCTTTTCATAGGAGGGGG	617		

RESULT 30  
BU404431  
BU404431  
BU404431 418 bp mRNA linear EST 27-NOV-2002  
604138647F1 CSEQCHN59 Gallus gallus cDNA clone CHEST967n11 5', mRNA  
sequence.

sequence.  
 ACCESSION BU404431  
 VERSION BU404431.1 GI:25773487  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus;  
 1 (bases 1 to 418)  
 Boardman, P. E., Saz-Exquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,  
 Fong W. T., Tickle, C. Brown, W. A., Wilson, S. A. and Hubbard, S. J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 12445392  
 Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)

PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

```

FEATURES
    source
        1..418
            Location/Qualifiers
                organism="Gallus gallus"
                mol_type="mRNA"
                strain="White Leghorn, Hisex"
                db_xref="taxon:9031"
                clones="CHEST967n11"
                dev_stage="36"
                lab_host="DH10B"
                clone_lib="CS3QCHN59"
                note="Organ: limbs; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al.. PNAS

```

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 16.8%; Score 88; DB 13; Length 418;  
Best Local Similarity 90.4%; Pred. No. 2.6e-16;  
Matches 94; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGACCTAGGGTGTGTTAGGCGAAAGCGGGCTTCGGTTGTACCGGT 209  
|||  
Db 315 GCTTGACTGAGGGACCACTAGTATGTTATAGCGAAAGCGGGCTTCGGTTGTACCGGT 374  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTATTCGCTTTTGCATAGGGA 253  
|||  
Db 375 TAGGATCCCTCAGGATATAGTATTCGCTTTTGCATAGGGA 418  
|||

RESULT 31  
BU490064  
LOCUS 598 bp mRNA linear EST 30-NOV-2002  
DEFINITION 604132030F1 CSEQBN37 Gallus gallus cDNA clone ChEST960k8 5', mRNA sequence.  
ACCESSION BU490064  
VERSION BU490064.1 GI:25983641  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 598)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source  
1..598  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="ChEST960k8"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQBN37"  
/note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 16.8%; Score 88; DB 13; Length 598;  
Best Local Similarity 90.4%; Pred. No. 3e-16;  
Matches 94; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGACCTAGGGTGTGTTAGGCGAAAGCGGGCTTCGGTTGTACCGGT 209  
|||  
Db 495 GCTTGACTGAGGGACCACTAGTATGTTATAGCGAAAGCGGGCTTCGGTTGTACCGGT 554  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTATTCGCTTTTGCATAGGGA 253  
|||  
Db 555 TAGGATCCCTCAGGATATAGTATTCGCTTTTGCATAGGGA 598  
|||

RESULT 32  
BU487895  
LOCUS 773 bp mRNA linear EST 30-NOV-2002  
DEFINITION 604126611F1 CSEQBN36 Gallus gallus cDNA clone ChEST946f3 5', mRNA sequence.  
ACCESSION BU487895  
VERSION BU487895.1 GI:25981472  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 773)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source  
1..773  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="ChEST946f3"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQBN36"  
/note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 16.8%; Score 88; DB 13; Length 773;  
Best Local Similarity 90.4%; Pred. No. 3.3e-16;  
Matches 94; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGGACCTAGGGTGTGTTAGGCGAAAGCGGGCTTCGGTTGTACCGGT 209

Db	47	TAGGAGTCCCTCCAGGATATAGTAGTTCGCCTTTTGCAGAAAGGAGTG	1
RESULT 34			
BU415406			
LOCUS	282 bp	mRNA	linear
DEFINITION	6036701171	CSEQRBL06	Gallus gallus CDNA clone CHES7613a5 5', mRNA
ACCESSION	BU415406		sequence.
VERSION	BU415406.1	GI:25908077	
KEYWORDS	EST.		
SOURCE	Gallus gallus	(chicken)	
ORGANISM	Gallus gallus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
AUTHORS	Boardman,P.R.; Sanz-Ezquerro,J.; Overton,I.M.; Burt,D.W.; Bosch,E.; Fong,W.T.; Tickle,C.; Brown,W.R.A.; Wilson,S.A. and Hubbard,S.J.		
TITLE	A Comprehensive Collection of Chicken cDNAs		
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)		
MEDLINE	22335534		
PUBMED	12445392		
COMMENT	Contact: Simon Hubbard		
	Department of Biomolecular Sciences		
	University of Manchester Institute of Science and Technology		
	(UMIST)		
	PO Box 88, Manchester, M60 1QD, UK		
	Tel: 01612008910		

```

FEATURES
    source
        1. .282
            Location/Qualifiers
                taxon="Callus gallus"
                mol_type="mRNA"
                strain="Layer and broiler"
                db_xref="taxon:9031"
                clone="ChrST613a5"

```

```

/qd_xref="taxon:9031"
/clone="ChEST613a5"
/sex="Male and female"
/tissue type="Abdominal fat pad"
/dev stage="adult"
/lab_host="DH108"
/clone_lib="CSEORBL06"
/note=Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'cgccgctgcagccgcgcgaaaaag;
[5'aattctttttgcagcggtgcagc]]

```

Query Match 16.5%; Score 86.4; DB 13; Length 282;  
 Best local Similarity 93.8%; Pred. No. 7e-16;  
 Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0  
 QY 181 CGAAAGCGGGGTTTCGGTTGTACGCGGTAGGAGTCCCTCAGGATATAGTTTGGC 240

[illegible]



ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BU471721  
BU471721.1 GI:25965298  
EST.  
Gallus gallus (chicken)

ORGANISM

Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 766)

AUTHORS

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs

JOURNAL

Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE

22335534

PUBMED

12445392

COMMENT

Contact: Simon Hubbard  
Department of Biochemical Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1. .766  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Laver"  
/db\_xref="taxon:9031"  
/clone="CHEST571116"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQB21"

/note="Organ: ovary; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; this normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

ORIGIN

Query Match 16.5%; Score 86.4; DB 13; Length 766;  
Best Local Similarity 89.4%; Pred. No. 1e-15;  
Matches 93; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGCGACTAGGTCGTCTTAGCGGAAAGCGGGCTTCGGTTGACGGGT 209  
|||  
Db 108 GCTTGACTGAGGGGACCATAGTATGTATAGCGGAAAGCGGGGCTTCGGTTGACGGGT 49  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTTCGCTTTTCATAGGGA 253  
|||  
Db 48 TAGGAGTCCCTCAGGATATAGTTCGCTTTTCATAGGGA 5  
|||

RESULT 36

BU243776

LOCUS

BU243776 780 bp mRNA linear EST 26-NOV-2002

DEFINITION

603781634F1 CSEQCHN34 Gallus gallus cDNA clone CHEST731c9 5', mRNA

ACCESSION

sequence.

BU243776

VERSION

BU243776.1 GI:25491080

KEYWORDS

EST.

SOURCE

Gallus gallus (chicken)

ORGANISM

Gallus gallus

REFERENCE

AUTHORS

1 (bases 1 to 780)

TITLE

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs

JOURNAL

Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE

22335534

PUBMED

12445392

COMMENT

Contact: Simon Hubbard  
Department of Biochemical Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1. .780  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST731c9"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN34"  
/note="Organ: liver; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

ORIGIN

Query Match 16.5%; Score 86.4; DB 13; Length 780;  
Best Local Similarity 85.7%; Pred. No. 1.1e-15;  
Matches 96; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 150 GCGTATCTGAGGCGACTAGGTCGTCTTAGCGGAAAGCGGGCTTCGGTTGACGGGT 209  
|||  
Db 498 GCTTGACTGAGGGGACCATAGTATGTATAGCGGAAAGCGGGGCTTCGGTTGACGGGT 557  
|||

QY 210 TAGGAGTCCCTCAGGATATAGTTCGCTTTTCATAGGAGGGGAAA 261  
|||  
Db 558 TAGGAGTCCCTCAGGATACAGTAGTTCGCTTTATGCAATAGCGAGGGGAAA 609  
|||

RESULT 37

BU349048

LOCUS

BU349048 269 bp mRNA linear EST 28-NOV-2002

DEFINITION

604168720F1 CSEQCHN69 Gallus gallus cDNA clone CHEST102895 5', mRNA

ACCESSION

sequence.

BU349048

VERSION

BU349048.1 GI:25857049

KEYWORDS

EST.

SOURCE

Gallus gallus (chicken)

ORGANISM

Gallus gallus

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 269)

AUTHORS

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,



Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@unist.ac.uk.

# FEATURES

source

Location/Qualifiers  
1. .516  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST992f15"  
/tissue\_type="whole embryo"  
/dev\_stage="20-21"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN03"  
/note="Organ: whole embryo; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 14.5%; Score 76; DB 13; Length 516;  
Best Local Similarity 89.4%; Pred. No. 1.6e-12;  
Matches 93; Conservative 0; Mismatches 10; Indels 1; Gaps 1;  
Qy 150 GGTATCTGAGGGAGTGGTGTAGGCGAAAGCGGGGCTTCGGTTGACGGGT 209  
Db 414 GCTTGACTGAGGGAGCCATGATGATAGGCGAAGGC-GGGCTTCGGTTGACGGGT 472  
Qy 210 TAGGAGTCCCTCAGGATATAGTTCGCTTTTCATAGGGA 253  
Db 473 TAGGAGTCCCTCAGGATATAGTTCGCTTTTCATAGGGA 516

RESULT 40  
BU491086 611 bp mRNA linear EST 30-NOV-2002  
LOCUS 604131646F1 CSQRB37 Gallus gallus cDNA clone CHEST959K12 5', mRNA  
DEFINITION sequence.  
ACCESSION BU491086  
VERSION BU491086.1 GI:25984663  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 611)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@unist.ac.uk.

## FEATURES

source

/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST959K12"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQR37"  
/note="Organ: pancreas; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 14.3%; Score 74.8; DB 13; Length 611;  
Best Local Similarity 87.5%; Pred. No. 4.2e-12;  
Matches 105; Conservative 0; Mismatches 12; Indels 3; Gaps 2;  
Qy 150 GGTATCTGAGGGAGTGGTGTAGGCGAAAGCGGGGCTTCGGTTGACGGGT 209  
Db 485 GCTTGACTGAGGGAGCCATGATGATAGGCGAAGGC-GGGCTTCGGTTGACGGGT 543  
Qy 210 TAGG-AGTCCCTCAGGATATAGTTCGCTTTTCATAGGAGGGGAAATAGT 267  
Db 544 TAGGAGTCCCTCAGGATATAGTTCGCTTTTCATAGGAGGGGAAATAGT 603

## RESULT 41

BU491487 647 bp mRNA linear EST 30-NOV-2002  
LOCUS 604130736F1 CSQRB37 Gallus gallus cDNA clone CHEST9579 5', mRNA  
DEFINITION sequence.  
ACCESSION BU491487  
VERSION BU491487.1 GI:25985064  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 647)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@unist.ac.uk.

## FEATURES

source

Location/Qualifiers  
1. .647  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST9579"

/sex="Male and female"  
 /dev stage="adult"  
 /lab host="DH10B"  
 /clone lib="CSPQR3N37"  
 /note="Organ: pancreas; Vector: pBluescript II KS(+);  
 Site 1: EcoRI; Site 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand synthesis reaction,  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 14.1%; Score 73.8; DB 13; Length 647;  
 Best Local Similarity 84.1%; Pred. No. 8.9e-12;  
 Matches 95; Conservative 0; Mismatches 17; Indels 1; Gaps 1;  
 QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTAGCGGAAAGCGGGCTTCGGTTCACGGGT 209  
 Db 485 GCTTGACGTAGGGGACCAAGTATGTATAGGCGAAAGCGGGCTTCGGTTCACGGGT 544  
 QY 210 TAGGAGTCCCTCAGGATATAGTATGTTTC-GCTTTTGATAGGCGGGGAA 261  
 Db 545 TAGGAGTCCCTCAGGATATAGTATGTTTC-GCTTTTGATAGGCGGGGAA 597

## RESULT 42

BU232252  
 LOCUS 774 bp mRNA linear EST 26-NOV-2002  
 DEFINITION 603410762F1 CSPQCHN24 Gallus gallus cDNA clone CHEST327116 5', mRNA  
 sequence.  
 ACCESSION BU232252  
 VERSION BU232252.1 GI:25474766  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (Bases 1 to 774)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..774  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST327116"  
 /dev\_stage="22"  
 /lab\_host="DH10B"  
 /clone\_lib="CSPQCHN24"  
 /note="Organ: head; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand synthesis reaction,  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 13.8%; Score 72.4; DB 13; Length 774;  
 Best Local Similarity 83.6%; Pred. No. 2.6e-11;  
 Matches 107; Conservative 0; Mismatches 16; Indels 5; Gaps 2;  
 QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTAGCGGAAAGCGGGCTTCGGTTCACGG 205  
 Db 513 GCTTGACGTAGGGGACCAAGTATGTATAGGCGAAAGCGGGCTTCGGTTCACGG 672  
 QY 206 CGGTAGGAGTCCCTCAGGATAT-AGTAGTTCGGCTTTGATAGGCGGGGAAATGT 264  
 Db 673 CGGTAGGAGTCCCTCAGGATATAGTAGTTCGGCTTTGATAGGCGGGGAAATGT 732  
 QY 265 AGTCTTAT 272  
 Db 733 AGTCCAAT 740

## RESULT 43

BU416333  
 LOCUS 829 bp mRNA linear EST 29-NOV-2002  
 DEFINITION 603671314F1 CSEQRBL07 Gallus gallus cDNA clone CHEST616K3 5', mRNA  
 sequence.  
 ACCESSION BU416333  
 VERSION BU416333.1 GI:25909004  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (Bases 1 to 829)  
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..829  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHEST616K3"  
 /sex="Male and female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQRBL07"  
 /note="Organ: pancreas; Vector: pBluescript II KS(+);  
 Site 1: EcoRI; Site 2: NotI; Modification of pBluescript  
 II KS(+) [Stratagene] vector to accommodate cDNA produced

with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BspI and BamHI sites  
[5'aattcttttttcggatccggggtgcagc]

ORIGIN

Query Match 13.6%; Score 71; DB 13; Length 829;  
Best Local Similarity 89.2%; Pred. No. 7.3e-11;  
Matches 99; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
  
QY 156 CTGAGGGACATAGGTGTGTT-TAGGCGAAAGCGGG-CTTCGGTTGTACGGGTTAGG 213  
Db CTGAGGGACCATAGTATGTTATAGCGAAAGCGGGCTTCGGTTGTACGGGTTAGG 767  
  
QY 214 ACTCCCTCAGGATATAGTTCGCTTTTGCATAGGAGGGGGAATGT 264  
Db AGTCCCTCAGGATATAGTTCGCTTTTGCATAGGAGGGGGAATGT 818

RESULT 44

BU315394 773 bp mRNA linear EST 28-NOV-2002  
LOCUS 603853390F1 CSEQCHN62 Gallus gallus cDNA clone CHEST853c24 5', mRNA  
DEFINITION sequence.  
ACCESSION BU315394  
VERSION BU315394.1 GI:25823395  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 773)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source  
1..773  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hixes"  
/db\_xref="taxon:9031"  
/clone="CHEST853c24"  
/dev\_stage="36"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN62"  
/note="Organ: heads; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6

(1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 13.5%; Score 70.4; DB 13; Length 773;  
Best Local Similarity 83.3%; Pred. No. 1.1e-10;  
Matches 80; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
  
QY 161 GGGACATAGGTGTGTTTAGCGGAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCC 220  
Db GGGACATAGGTGTGTTTAGCGGAAAGCGGGCTTCGGTTGTACGGGTTAGGATCCCC 737  
  
QY 221 TCAGGATATAGTTCGCTTTTGCATAGGAGGG 256  
Db TCAGGATATAGTTCGCTTTTGCATAGGAGGG 773

RESULT 45

BU490009 642 bp mRNA linear EST 30-NOV-2002  
LOCUS 604129112F1 CSEQCHN37 Gallus gallus cDNA clone CHEST953g3 5', mRNA  
DEFINITION sequence.  
ACCESSION BU490009  
VERSION BU490009.1 GI:25983586  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 642)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source  
1..642  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST953g3"  
/sex="Male and female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN37"  
/note="Organ: pancreas; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 13.4%; Score 70; DB 13; Length 642;

Best Local Similarity 89.3%; Pred. No. 1.4e-10;  
Matches 109; Conservative 0; Mismatches 10; Indels 3; Gaps 3;  
QY 150 GCGTATCTAGGGGACTAGGCTGTGTTAGCGGAAAGCGGGCTTCGG-TTGTAGCGCG 208  
Db 503 GCTTACTGAGGGGACCATAGTATGTATAGCGGAAAGCGGGCTTCGGTTGTAGCGCG 562  
QY 209 TTAGGAGT-CCCTCAGGATATAGTAGTTTGC-TTTTGCATAGGAGGGGAAATGTAG 266  
Db 563 TTAGGAGTCCCTCAGGATATAGTAGTTTGCCTTTTGCATAGGAGGGGAAATGTAG 622  
QY 267 TC 268  
Db 623 TC 624

RESULT 46  
BU350008  
LOCUS 603526141F1 CSEQCHN69 848 bp mRNA linear EST 28-NOV-2002  
DEFINITION 603526141F1 CSEQCHN69 Gallus gallus cDNA clone CHEST473all 5', mRNA  
sequence.  
ACCESSION BU350008  
VERSION BU350008  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 848)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..848  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST473all"  
/sex="Female"  
/tissue\_type="cerebellum"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN69"  
/note="Organ: brain; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 13.3%; Score 69.8; DB 13; Length 848;  
Best Local Similarity 89.3%; Pred. No. 1.4e-10;  
Matches 109; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

Best Local Similarity 87.6%; Pred. No. 1.8e-10;  
Matches 99; Conservative 0; Mismatches 12; Indels 2; Gaps 2;  
QY 161 GGGACTAGGCTGTGTTAGCGGAAAGCGGGCTTCGGTTGTACGGGTAGGAGTCCC 220  
Db 625 GGGACATAGTATGATATAGCGGAAAGCGGGCTTCGGTTGTACGGGTAGGAGT-CCC 683  
QY 221 TCAGGATATAGTAGTTTGCCTTTTGCAT-AGGGAGGGGGAANTGTAGTCTTAT 272  
Db 684 TCAGGATATAGTAGTTTGCCTTTTGCATAGGAGGGGGAACATGTAGTACAT 736

RESULT 47  
BU403961  
LOCUS 603482276F1 CSEQCHN59 851 bp mRNA linear EST 27-NOV-2002  
DEFINITION 603482276F1 CSEQCHN59 Gallus gallus cDNA clone CHEST371520 5', mRNA  
sequence.  
ACCESSION BU403961  
VERSION BU403961  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 851)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..851  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST371520"  
/dev\_stage="36"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN59"  
/note="Organ: limbs; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 13.2%; Score 69.2; DB 13; Length 851;  
Best Local Similarity 86.8%; Pred. No. 2.7e-10;  
Matches 99; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 150 GCGTATCTAGGGGACTAGGCTGTGTTAGCGGAAAGCGGGCTTCGGTTGTAGCGGT 209  
Db 635 GCTTACTAGGAGGGGACCATAGTATGTATAGCGGAGCGGGCTTCGGATGTAGCGGT 694

QY 210 TAGGAGTCCCTCAGGATA-TAGTAGTTTCGCTTT-GCATAGGAGGGGAAA 261  
 Db |||||  
 695 TAGGAGTCCCTCAGGATA-TAGTAGTTTCGCTTT-GCATAGGAGGGGAAA 748  
 |||||

RESULT 49  
 A1981988  
 LOCUS 647 bp mRNA linear EST 07-MAY-2001  
 DEFINITION pat.pk0070.g7.f chicken activated T cell cDNA Gallus gallus cdna  
 ACCESSION clone.pat.pk0070.g7.f 5' similar to protein v-src, mRNA sequence.  
 A1981988  
 VERSION MEDLINE  
 KEYWORDS PUBMED  
 SOURCE EST.  
 ORGANISM A1981988.1 GI:5985016  
 Gallus gallus (chicken)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 647)  
 Tirunaguru,V.G., Sofer,L., Cui,J. and Burnside,J.  
 An expressed sequence tag database of T-cell-enriched activated  
 chicken splenocytes: sequence analysis of 5251 clones  
 Genomics 66 (2), 144-151 (2000)  
 MEDLINE 20318616  
 PUBMED 10860659  
 COMMENT Contact: Joan Burnside  
 Molecular Endocrinology  
 University of Delaware  
 40 Townsend Hall, Newark, DE 19717, USA  
 Tel: 302 831-1345  
 Fax: 302-831-3411  
 Email: joan@udel.edu, www.chickest.udel.edu  
 Seq primer: 87.

FEATURES  
 source  
 1..647  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="pat.pk0070.g7.f"  
 /sex="male"  
 /cell\_type="Con A-activated splenic T cell"  
 /lab\_host="E.coli TOP10 P"  
 /clone\_lib="chicken activated T cell cdna"  
 /note="vector: pcdNA3"

ORIGIN  
 Query Match 13.08; Score 68.2; DB 9; Length 647;  
 Best Local Similarity 69.28; Pred. No. 5e-10;  
 Matches 119; Conservative 0; Mismatches 51; Indels 2; Gaps 2;  
 QY 158 GAGGGGACTAGGGTGTGTTTGGCGAAAGCGGGGCTTCGGTTGTACGCGTTTAGGATC 217  
 |||||  
 Db 407 GAGGGGACCATAGTATGTATAGCGAAAGCGGGGCTTCGGTTGTACGCGTTTAGGATC 466  
 |||||  
 QY 218 CCTCAGGATATAGTGTGTTTCGCTTTGATAGGAGGGGGAATGTCTTATGCA 276  
 |||||  
 Db 467 CCTCAGGATACATAGTGTGCGGCTTAAGCATAGGAGGGGGAATGTATCAATAGA 526  
 |||||  
 QY 277 TACTCTTGTAGTCTTGCACATGTGTAAGTATGATTTAGCAACATGCGCTTACA 328  
 |||||  
 Db 527 GCCAGAGCA-ACINGAATATCTTAAGACNATATAGGAAAGCAAGACA 577  
 |||||

RESULT 49  
 BU402803  
 LOCUS 630 bp mRNA linear EST 27-NOV-2002  
 DEFINITION 603485204F1 CSEQCHN59 Gallus gallus cdna clone CHEST378h1 5', mRNA  
 sequence.  
 ACCESSION BU402803  
 VERSION BU402803.1 GI:25771859  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 630)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: simon.hubbard@umist.ac.uk.

FEATURES  
 source  
 1..630  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST378h1"  
 /dev\_stage="36"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN59"  
 /note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:  
 EcoRI; Site 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunt-ended, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Ronaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

ORIGIN  
 Query Match 12.78; Score 66.6; DB 13; Length 630;  
 Best Local Similarity 81.18; Pred. No. 1.6e-09;  
 Matches 90; Conservative 0; Mismatches 19; Indels 2; Gaps 1;  
 QY 150 GCCTATCTCAGGGGACTAGGGTGTGTTTGGCGAAAGCGGGGCTTCGGTTGTACGCG- 208  
 |||||  
 Db 462 GCTTGACTGAGGGGACCATAGTATGTATAGCGAAGCGGGGCTTCGGTTGTACGCGC 521  
 |||||  
 QY 209 -TTAGAGTCCCTCAGGATATAGTATTCGCTTTTGCATAGGAGGGGG 258  
 |||||  
 Db 522 TTCAGGAGTCCCTCAGGATATAGTATTCGCGCTTTTCGCAATAGGAGGGG 572  
 |||||

RESULT 50  
 BU416401  
 LOCUS 619 bp mRNA linear EST 29-NOV-2002  
 DEFINITION 603551243F1 CSEQREL07 Gallus gallus cdna clone CHEST521e12 5', mRNA  
 sequence.  
 ACCESSION BU416401  
 VERSION BU416401.1 GI:25909072  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 619)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,





/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Obese Strain (OS)"  
/db\_xref="taxon:9031"  
/clone="H29"  
/sex="male and female"  
/tissue\_type="thyroid"  
/clone\_lib="Chicken thyroid SSH library"  
/note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system (Qiagen), and used for SSH. Hybridisation was performed using the PCR-select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

## ORIGIN

Query Match 12.1%; Score 63.2; DB 13; Length 195;  
Best Local Similarity 95.6%; Pred. No. 1.1e-08;  
Matches 65; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 205 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 264  
Db 195 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 136  
QY 265 AGTCTTAT 272  
Db 135 AGTCAAAAT 128

RESULT 53  
BQ839776/c  
LOCUS BQ839776 195 bp mRNA linear EST 09-AUG-2002  
DEFINITION H30 chicken thyroid SSH library Gallus gallus cDNA clone H30  
similar to Avian leukosis virus strain ev-3, mRNA sequence.

ACCESSION BQ839776  
VERSION BQ839776.1 GI:22165703  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 195)  
AUTHORS Vasicek,D., Kaiser,P. and Hala,K.  
TITLE Analysis of expressed sequence tags from the thyroid glands of chickens affected with spontaneous autoimmune thyroiditis, an animal model of human Hashimoto's thyroiditis

JOURNAL Unpublished (2002)

COMMENT Contact: Kaiser P  
Institute for Animal Health  
Compton, Berkshire RG20 7NN, UK  
Tel: +44 1635 577263  
Fax: +44 1635 577263  
Email: pete.kaiser@bsrc.ac.uk  
Seq primer: T7.

## FEATURES

Location/Qualifiers  
1..195  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Obese Strain (OS)"  
/db\_xref="taxon:9031"  
/clone="H30"

/sex="male and female"  
/tissue\_type="thyroid"

/clone\_lib="Chicken thyroid SSH library"

/note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system

## ORIGIN

Query Match 12.1%; Score 63.2; DB 13; Length 195;  
Best Local Similarity 95.6%; Pred. No. 1.1e-08;  
Matches 65; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 205 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 264  
Db 195 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 136  
QY 265 AGTCTTAT 272  
Db 135 AGTCAAAAT 128

## RESULT 54

BQ839779/c

LOCUS BQ839779 195 bp mRNA linear EST 09-AUG-2002  
DEFINITION E31 Chicken thyroid SSH library Gallus gallus cDNA clone E31  
similar to Avian leukosis virus strain ev-3, mRNA sequence.

ACCESSION BQ839779

VERSION BQ839779.1 GI:22165706

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 195)

AUTHORS Vasicek,D., Kaiser,P. and Hala,K.

TITLE Analysis of expressed sequence tags from the thyroid glands of chickens affected with spontaneous autoimmune thyroiditis, an animal model of human Hashimoto's thyroiditis

JOURNAL Unpublished (2002)

COMMENT Contact: Kaiser P

Institute for Animal Health  
Compton, Berkshire RG20 7NN, UK  
Tel: +44 1635 577263

Fax: +44 1635 577263

Email: pete.kaiser@bsrc.ac.uk

Seq primer: T7.

Location/Qualifiers

1..195

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Obese Strain (OS)"

/db\_xref="taxon:9031"

/clone="E31"

/sex="male and female"

/tissue\_type="thyroid"

/clone\_lib="Chicken thyroid SSH library"

/note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system (Qiagen), and used for SSH. Hybridisation was performed using the PCR-select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

## ORIGIN

Query Match 12.1%; Score 63.2; DB 13; Length 195;  
Best Local Similarity 95.6%; Pred. No. 1.1e-08;  
Matches 65; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 205 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 264  
Db 195 GCGTTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGGGGGAATGT 136

(Qiagen), and used for SSH. Hybridisation was performed using the PCR-select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

QY 265 AGTCTTAT 272  
 DB 135 AGTCAGAT 128

RESULT 55  
 BU414765  
 LOCUS 844 bp mRNA linear EST 29-NOV-2002  
 DEFINITION 603667837F1 CSEQRL06 Gallus gallus cdna clone CHES760710 5', mRNA sequence.  
 ACCESSION BU414765  
 VERSION BU414765.1 GI:25907436  
 KEYWORDS EST.  
 ORGANISM Gallus gallus (chicken)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; 1 (bases 1 to 844)  
 REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)  
 JOURNAL MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
 source  
 1..844  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHEST60710"  
 /sex="Male and female"  
 /tissue\_type="Abdominal fat pad"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQRL06"  
 /notes="Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BglI and BamHI sites (5'ggcgcgtgcagcccggtatccgaaaaaag| |5'aattcttttttcgggtccgggctgcagc|)"

ORIGIN  
 Query Match 12.0%; Score 62.8; DB 13; Length 844;  
 Best Local Similarity 79.1%; Pred. No. 2.8e-08;  
 Matches 87; Conservative 0; Mismatches 22; Indels 1; Gaps 1;  
 QY 150 GGTATCTAGAGGGGATAGGGTGTGTTAGGCGAAGCGGGCTTCGGTTTACGGGT 209  
 DB 682 GCTTCACTAGGGGACCATAGTAATGTATAGGCGAAGCGGGCTCGGTTTACGGGT 741  
 QY 210 TAGGAGTCCCTCAGATATAGTAG-TTTCGCTTTTCATAGGAGGGG 258  
 DB 742 TAGGAGTCCCTCAGATATAGTAGTTCGCTTTTCATAGGAGGGG 791

RESULT 56  
 BQ839752/c

LOCUS BQ839752  
 DEFINITION H24 Chicken thyroid SSH library Gallus gallus cdna clone H24 similar to Avian leukosis virus strain ev-3, mRNA sequence.  
 ACCESSION BQ839752  
 VERSION BQ839752.1 GI:22165679  
 KEYWORDS EST.  
 ORGANISM Gallus gallus (chicken)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; 1 (bases 1 to 197)  
 REFERENCE Vasicek, D., Kaiser, P. and Hala, K. Analysis of expressed sequence tags from the thyroid glands of chickens affected with spontaneous autoimmune thyroiditis, an animal model of human Hashimoto's thyroiditis  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kaiser P  
 Institute for Animal Health  
 Compton, Berkshire RG20 7NN, UK  
 Tel: +44 1635 577263  
 Fax: +44 1635 577263  
 Email: pete.kaiser@ahrc.ac.uk  
 Seq primer: 17.

FEATURES  
 source  
 1..197  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Obese Strain (OS)"  
 /db\_xref="taxon:9031"  
 /clone="H24"  
 /sex="male and female"  
 /tissue\_type="thyroid"  
 /clone\_lib="Chicken thyroid SSH library"  
 /note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system (Qiagen), and used for SSH. Hybridisation was performed using the PCR-Select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

ORIGIN  
 Query Match 11.9%; Score 62; DB 13; Length 197;  
 Best Local Similarity 92.9%; Pred. No. 2.7e-08;  
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 203 ACCGGTTAGGAGTCCCTCAGGATATAGTTTCGCTTTTCATAGGAGGGGGAAT 262  
 DB 197 ACGCGTTAGGAGTCCCTCAGGATATAGTTTCGCTTTTCATAGGAGGGGGAAT 138  
 QY 263 GTAGTCTTAT 272  
 DB 137 GTAGTCAAAAT 128

RESULT 57  
 BQ839750/c

LOCUS BQ839750  
 DEFINITION E24 Chicken thyroid SSH library Gallus gallus cdna clone E24 similar to Avian leukosis virus strain ev-3, mRNA sequence.  
 ACCESSION BQ839750  
 VERSION BQ839750.1 GI:22165677  
 KEYWORDS EST.  
 ORGANISM Gallus gallus (chicken)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; 1 (bases 1 to 196)  
 REFERENCE Vasicek, D., Kaiser, P. and Hala, K.

**TITLE** Analysis of expressed sequence tags from the thyroid glands of chickens affected with spontaneous autoimmune thyroiditis, an animal model of human Hashimoto's thyroiditis, an unpublished (2002)

**JOURNAL COMMENT**  
Contact: Kaiser P  
Institute for Animal Health  
Compton, Berkshire RG20 7NN, UK  
Tel: +44 1635 577263  
Fax: +44 1635 577263  
Email: pete.kaiser@bbsrc.ac.uk  
Seq primer: T7:

# **FEATURES**

**source**  
1. .196  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Obese Strain (OS)"  
/db\_xref="taxon:9031"  
/clone="E24"  
/sex="male and female"  
/tissue\_type="thyroid"  
/note="RNA was prepared from the thyroids of OS birds, which go on to suffer from spontaneous autoimmune thyroiditis, and those of control CB strain birds, using TRI Reagent. This was then enriched for polyadenylated RNA molecules using the Oligotex mRNA purification system (Qiagen), and used for SSH. Hybridisation was performed using the PCR-Select cDNA subtraction kit and the Advantage cDNA Polymerase Mix (both Clontech). Forward and reverse subtractions were performed."

# **ORIGIN**

**Query Match** 11.5%; Score 60; DB 13; Length 196;  
**Best Local Similarity** 92.6%; Pred. No. 1.2e-07;  
**Matches** 63; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 205 GCGGTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTCATGAGGAGGGAATCT 264  
**Db** 196 GCGGTAGAGTCCCTCAGGATATAGTAGTTTCGCTTTTCATGAGGAGGGAATCT 137

**QY** 265 AGTCTTAT 272  
|||||  
**Db** 136 AGTCAAT 129

**RESULT 58**  
**BU314089**  
**LOCUS** BU314089.1 751 bp mRNA linear EST 28-NOV-2002  
**DEFINITION** 603544624F1 CSEQCHN61 Gallus gallus cDNA clone CHST51906 5', mRNA sequence.

**ACCESSION** BU314089  
**VERSION** BU314089.1 GI:25822090  
**KEYWORDS** EST.  
**SOURCE** Gallus gallus (chicken)

**ORGANISM** Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

**REFERENCE** 1 (bases 1 to 751)  
**AUTHORS** Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
**TITLE** A Comprehensive Collection of Chicken cDNAs  
**JOURNAL** Curr. Biol. 12 (22), 1965-1969 (2002)  
**MEDLINE** 22335534  
**PUBMED** 12445392

**COMMENT**  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

# **FEATURES**

**source**  
1. .751  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="ChST51906"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN61"

/note="Organ: heart; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; this normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

# **ORIGIN**

**Query Match** 10.8%; Score 56.6; DB 13; Length 751;  
**Best Local Similarity** 87.3%; Pred. No. 2.3e-06;  
**Matches** 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

**QY** 150 GCGTATCTGAGGGGACTAGGTGTGTTAGCGGAAAGCGGGCTTCGGTGTACGGCGT 209  
**Db** 680 GCTTCGACTGAGGGGACCATAGTAGTATAGCGGAAAGCGGGCTTCGGTGTACGGCGT 739

**QY** 210 TAGGAGTCCCC 220  
|||||  
**Db** 740 TAGGAGTCCCC 750

**RESULT 59**  
**BU124247**  
**LOCUS** BU124247.1 945 bp mRNA linear EST 25-NOV-2002  
**DEFINITION** 603148493F1 CSEQCHL18 Gallus gallus cDNA clone CHST151124 5', mRNA sequence.

**ACCESSION** BU124247  
**VERSION** BU124247.1 GI:25334922  
**KEYWORDS** EST.  
**SOURCE** Gallus gallus (chicken)

**ORGANISM** Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

**REFERENCE** 1 (bases 1 to 945)  
**AUTHORS** Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
**TITLE** A Comprehensive Collection of Chicken cDNAs  
**JOURNAL** Curr. Biol. 12 (22), 1965-1969 (2002)  
**MEDLINE** 22335534  
**PUBMED** 12445392

**COMMENT**  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

**FEATURES**  
**source**  
1. .945  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"

/db\_xref="taxon:9031"  
 /clone="CHEST151i24"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSQCHL18"  
 /note="Organ: small intestine; Vector: pBluescript II  
 KS(+); Site 1: EcoRI; Site 2: NotI; Modification of  
 pBluescript II KS(+) [Stratagene] vector to accommodate  
 cDNA produced with the T-trimmed protocol (Construction of  
 uni-directionally cloned cDNA libraries from messenger RNA  
 for improved 3' end DNA sequencing by Glenn Fu, et al.  
 U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with  
 NotI and EcoRI. Ligate in double stranded adaptor  
 containing BspI and BamHI sites  
 [5'ggcggctgcagcccgatccgaaaaaag]  
 [5'aattcttttttcggatccgggggtgcacgc]"

## ORIGIN

Query Match 10.7%; Score 55.8; DB 13; Length 945;  
 Best Local Similarity 82.2%; Pred. No. 4.5e-06;  
 Matches 88; Conservative 0; Mismatches 17; Indels 2; Gaps 2;  
 QY 156 CTGAGGGGACTAGGGTGTGTTAGCGGAAAGCGGGCTTCGGTTGACCGGTTAGGAG 215  
 Db 696 CTGAGGGGACCATAGTATGTATAGCG-AAAGGGGGGCTTCGGTTGACCGGTTAGGAG 754  
 QY 216 TCCCTCAGGA-TATAGTAGTTGCTTTTGCATAGGAGGGGAAA 261  
 Db 755 TCTCTCAGGTACAGTAGTGCCTTATGATAGGAGGGGGGAA 801

RESULT 60  
 BU406314  
 LOCUS 576 bp mRNA linear EST 27-NOV-2002  
 DEFINITION 604140918F1 CSQCHN59 Gallus gallus cDNA clone CHEST973d6 5', mRNA  
 sequence.  
 ACCESSION BU406314  
 VERSION BU406314.1 GI:25775370  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 576)  
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..576  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST973d6"  
 /dev\_stage="36"  
 /lab\_host="DH10B"  
 /clone\_lib="CSQCHN59"  
 /note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:  
 EcoRI; Site 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was bluntended, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 10.6%; Score 55.6; DB 13; Length 576;  
 Best Local Similarity 87.1%; Pred. No. 4.3e-06;  
 Matches 61; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 150 GCGTATCTGAGGGGACTAGGGTGTGTTAGCGGAAAAGCGGGCTTCGGTTGACCGGT 209  
 Db 502 GCTTGACTGAGGGGACCATAGTATGTATAGCGGAAAGCGGGCTTCGGTTGACCGGT 561  
 QY 210 TAGGAGTCCC 219  
 Db 562 TAGGAGTCCC 571

RESULT 61  
 BU470895/c  
 LOCUS 622 bp mRNA linear EST 30-NOV-2002  
 DEFINITION 603760965F1 CSQREN21 Gallus gallus cDNA clone CHEST679a18 5', mRNA  
 sequence.  
 ACCESSION BU470895  
 VERSION BU470895.1 GI:25964472  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 622)  
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source

1..622  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer"  
 /db\_xref="taxon:9031"  
 /clone="CHEST679a18"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSQREN21"  
 /note="Organ: ovary; Vector: pBluescript II KS(+); Site 1:  
 EcoRI; Site 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was bluntended, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI

```
Query Match      10.4%; Score 54.6; DB 13; Length 750;
Best Local Similarity 87.0%; Pred. No. 9.8e-06;
Matches 60; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

682 GCTTACTGAGGGACCA<sup>+</sup>TAGTATGTATAGCGAAGCGGGGCTTCGGTTGTACCGGT 741

742 TAGGAGTCC 750

RESULT 63

LOCUS	BU413106	747 bp	mRNA	linear	EST 29-NOV-2002
LOCUS	BU413106	747 bp	mRNA	linear	EST 29-NOV-2002

ORGANISM	Gallus gallus
EST.	Gallus gallus (chicken)
WORDS	Gallus gallus
ORGANISM	Gallus gallus

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

**AUTHORS**  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

JOURNAL  
CURR. BIOL. 12 (22), 1965-1969 (2002)  
MEDLINE  
0022-5534

COMMENT  
Contact: Simon Hubbard

University of Manchester Institute of Science and Technology

PO Box 88, Manchester, M60 1QD, UK  
TEL: 0161 200 8930

Fax: 01622 606105  
Email: Simon.Hubbard@umist.ac.uk.

source	1. .747
--------	---------

```
/mol_type="mrna"
/submit="yes"
/submit="yes"
```

```

/ww_xref="taxon:9031"
/clone="ChEST166b3"

```

```

/dev_stage="adult"

```

```

/clone_lib="CSEQRBL05"

```

ECOR1; Site 2: NOT1; MODIFICATION OF BUSINESSCRIPT II WS(7)  
[5] ratagene\_T vector to accommodate and produced with the

cloned cDNA libraries from messenger RNA for improved 3'

6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.

BamHI sites [5'ggccgctgcagcccgatccgaaaaag]  
[5'ggccgctgcagcccgatccgaaaaag]#

**RIGHT**

Best Local Similarity 94.8%; Pred. No. 2.7e-05;

[illegible]

*(The following text is extremely faint and largely illegible due to extreme blurring and low contrast. It appears to be a list or index of items, possibly related to the "List of Figures" mentioned in the caption.)*

Db 4 GTCCCTCAGATAGTAGTGGCTTTTGGCATAGGAGGGGAATAGTAGCAAT 61

RESULT 64  
LOCUS BU414993  
DEFINITION 603668991F1 CSEQRL06 Gallus gallus cDNA clone CHEST510e23 5', mRNA  
ACCESSION BU414993 767 bp mRNA linear EST 29-NOV-2002  
KEYWORDS 603668991F1 CSEQRL06 Gallus gallus cDNA clone CHEST510e23 5', mRNA  
SOURCE EST.  
ORGANISM Gallus gallus (chicken)  
REFERENCE 1 (bases 1 to 767)  
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..767  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST510e23"  
/sex="Male and female"  
/tissue\_type="Abdominal fat pad"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQRL06"  
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;  
Site 2: NotI; Modification of pBluescript-II KS(+)  
[Stratagene] vector to accommodate cDNA produced with the  
T-trimmed protocol (Construction of uni-directionally  
cloned cDNA libraries from messenger RNA for improved 3'  
end DNA sequencing by Glenn Fu, et al. U.S. Patent  
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
Ligate in double stranded adaptor containing BsgI and  
BamHI sites [5'ggcgggtgcagccgcgacccgagaaaaag]  
[5'aattcttttttcggatccg999ctgcagc]"

ORIGIN  
Query Match 9.9%; Score 51.8; DB 13; Length 767;  
Best Local Similarity 83.1%; Pred. No. 7.5e-05;  
Matches 59; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 150 GCCTATCTGAGGGACCTAGGCTGTGTTAGCGCAAGAGCGGCTTCGGTTGACCGGT 209  
|||  
Db 697 GCTTGACTGAGGGACCACTAGTATGTTGGCACAGCGGGGCTTCGGTTGACCGGT 756  
|||  
QY 210 TAGGAGTCCCC 220  
|||  
Db 757 TAGGAGTCCGC 767

RESULT 65  
CF252511  
LOCUS CF252511  
DEFINITION hdmn128\_a09 LPS-activated macrophage cell line Gallus gallus cDNA,  
mRNA sequence.

ACCESSION CF252511  
VERSION CF252511.1 GI:33485766  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
REFERENCE 1 (bases 1 to 725)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
Witzell,H.M., Bed'Hom,B., Morin,V., Young,J.R., Whittaker,C.J.,  
Chause,A.M. and Zoorob,R.  
TITLE A collection of chicken ESTs from activated immune cells  
JOURNAL Unpublished (2003)  
COMMENT Contact: Zoorob R  
UPR 1983  
CNRS  
7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
Tel: 33 1 49 58 35 00  
Fax: 33 1 49 58 33 81  
Email: zoorob@vjf.cnrs.fr.  
Location/Qualifiers  
1..725  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/cell\_line="HD11"  
/clone\_lib="LPS-activated macrophage cell line"  
/note="Vector: pTriplex2"

ORIGIN  
Query Match 9.0%; Score 47.2; DB 14; Length 725;  
Best Local Similarity 84.0%; Pred. No. 0.002;  
Matches 89; Conservative 0; Mismatches 13; Indels 4; Gaps 3;

QY 148 TCGCTATCTGAGGGGACTAGGCTGTGTTAGGCGAAAGC-GGGGCTTCGGTTGACGC 206  
|||  
Db 594 TGGCTTAACCTAGGCGGACTATGGCATGTATAGCGTAAGCGGGGCTTCGGTTGACGC 643  
|||  
QY 207 --GGTTAGAGTCCCTTC-AGGATATAGTGTTCGCTTTTGCA 249  
|||  
Db 644 CGGGTAGGAGTCCCTTAAGGATATAGTAGGCACGCTTTTGCA 689  
|||

RESULT 66  
BU490848  
LOCUS BU490848 718 bp mRNA linear EST 30-NOV-2002  
DEFINITION 604130845F1 CSEQRLN37 Gallus gallus cDNA clone CHEST957112 5', mRNA  
sequence.  
ACCESSION BU490848  
KEYWORDS BU490848.1 GI:25984425  
SOURCE EST.  
ORGANISM Gallus gallus (chicken)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 718)  
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers  
1..718

FEATURES  
source

```

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST957112"
/sex="Male and female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRN37"
/note="Organ: pancreas; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
ORIGIN
Query Match 8.9%; Score 46.8; DB 13; Length 718;
Best Local Similarity 88.6%; Pred. No. 0.0027;
Matches 62; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 156 CTGAGGGGACTAGGTGTGTAGCGAAAGCGGGCTTCGGTTGTACGGGTTAGGAG 215
Db 650 CTGAGGGGACCATATGATATAGCGAAAGCGGGCTTCGGTTGTACGGG-TAGGAG 708

Qy 216 TCCCTCAGG 225
Db 709 TCCCTCAGG 718

RESULT 67
BU414295 724 bp mRNA linear EST 29-NOV-2002
LOCUS 60368824F1 CSEQRN06 Gallus gallus CDNA clone CHEST609p5 5', mRNA
DEFINITION
sequence.
ACCESSION BU414295
VERSION BU414295.1 GI:25906953
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 724)
AUTHORS Boardman,P.E., Sanz-Exquerro,J., Overton,I.M., Burt,D.W., Bosch,B.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .724
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST609p5"

ORIGIN
source
Query Match 8.9%; Score 45.4; DB 9; Length 401;
Best Local Similarity 55.3%; Pred. No. 0.0059;
Matches 109; Conservative 0; Mismatches 86; Indels 2; Gaps 1;

Qy 185 AAGCGGGGCTTCGGTTGTACCGG--TTAGGAGTCCCTCAGGATATAGTAGTTTCGTT 242

```

```

/sex="Male and female"
/tissue_type="Abdominal fat pad"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRN06"
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggcgggtgcacccgcgacccgaaaaaag]
[5'aattcttttttcggatccgggggtgcacgc]"
ORIGIN
Query Match 8.9%; Score 46.6; DB 13; Length 724;
Best Local Similarity 79.5%; Pred. No. 0.0031;
Matches 93; Conservative 0; Mismatches 19; Indels 5; Gaps 3;

Qy 150 CGGTATCTAGGGGACTAGGTGTGTAGCGAAAGCGGGCTTCGG-TTGTACCGG 208
Db 537 GCTTGACTAGGGGACCATATGATATAGCGAAAGCGGGGCTTCGGTTGTACCGG 596

Qy 209 TTAGGAGTCCCTC--AGGATATAGTAGTTTCGC--TTTTGCATAGGAGGGGAAA 261
Db 597 TTAGGAAGTCCCTCAGGATATAGTAGTTTCGCGTTTTGCTAGGAGGGGGGAA 653

RESULT 68
AB083460 401 bp mRNA linear EST 12-APR-2002
LOCUS AB083460 Rattus norvegicus lactating adult Rattus norvegicus cDNA
DEFINITION clone VP60 3', similar to Myeloblastosis-associated virus type 2 env
gene (accession number: U10924.1), mRNA sequence.
ACCESSION AB083460
VERSION AB083460.1 GI:20144093
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 401)
AUTHORS Yamashita,M., Glasgow,E., Zhang,B., Kusano,K. and Gainer,H.
TITLE Identification of cell-specific mRNAs in oxytocinergic and
vasopressinergic magnocellular neurons in rat supraoptic nucleus by
single-cell differential hybridization
JOURNAL Unpublished (2002)
COMMENT Contact: Mitsuo Yamashita
Department of Biotechnology
Graduate School of Engineering, Osaka University
2-1 Yamadaoka, Suita, Osaka 565-0871, Japan
Tel: 81-6-6879-4170
Fax: 81-6-6879-7418
Email: yamashita@bio.eng.osaka-u.ac.jp.
Location/Qualifiers
1. .401
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="VP60"
/sex="female"
/dev_stage="lactating adult"
/clone_lib="Rattus norvegicus lactating adult"

ORIGIN
source
Query Match 8.7%; Score 45.4; DB 9; Length 401;
Best Local Similarity 55.3%; Pred. No. 0.0059;
Matches 109; Conservative 0; Mismatches 86; Indels 2; Gaps 1;

Qy 185 AAGCGGGGCTTCGGTTGTACCGG--TTAGGAGTCCCTCAGGATATAGTAGTTTCGTT 242

```

Query Match	8.38;	Score 43.4;	DB 13;	Length 575;
Best Local Similarity	82.0%;	Prod. No. 0.029,		
Matches 50;	Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0;
94	AATCTGCTTAGGGTTAGCGTTTTCGGCTGCTTCGGCGATGTACGGCCAGATATTCGGGT	153		
224	AATATATTTAGGATTAGGCGTTTTCGCTGCTTCGGCGATGTACGGGTTAGGTTGTGTGT	283		
154	A 154			
284	A 284			

		EST 08-MAY-2001
RESULT 70	EG711671	linear mRNA
	LOCUS	591 bp
	DEFINITION	pglin.pk008.m21 Normalized Liver Library Gallus gallus cDNA clone
		pglin.pk008.m21 5' similar to pir I50432 I50432 transmembrane
		protein - chicken (fragment) gb AA49106.1 (M95189) transmembrane
		protein [Gallus gallus]G_mRNA sequence.

```
FEATURES
SOURCE
LOCATION/Qualifiers
1. 581
/organism="Gallus gallus"
/mol type="mRNA"
/db xref="taxon:9031"
/clone="pgln.pk008.m21"
/sex="Male and Female"
/tissue type="liver"
/lab host="E.coli EMPH108"
/clone lib="Normalized Liver Library"
/note="vector: pCMVSPORT 6"
```

337 AATATATTAGGATTAGGCGTTTGGCGTGTCTCGCGATGACGGGTAGGTGTGTGTGT 396

RESULT 71					
BU258368					
LOCUS	608 bp	mRNA	linear	EST 26-NOV-2002	
DEFINITION	C603743103F1 CSEQCHN38 Gallus gallus cDNA clone CHES7643f1 5', mRNA				
	sequence.				
ACCESSION	BU258368				
VERSION	BU258368.1			GI:25521250	
KEYWORDS	EST.				

BU258368	608 bp	linear	EST 26-NOV-2002
LOCUS	603743103F1	CSE0QN38	Gallus gallus cDNA clone CHES7643f1 5', mRNA
DEFINITION	sequence.		
ACCESSION	BU258368		
VERSION	BU258368.1	GI:25521250	
KEYWORDS	EST.		



**AUTHORS** Jorge, E.C., Monteiro-Vitorello, C.B., Silva, C.S., Alves, H.J.,  
Patricio, M. and Coutinho, L.I.  
**TITLE** Discovery of new genes in chicken embryos  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Erika C. Jorge  
Laboratory of Animal Biotechnology, Dep. of Animal Production  
ESALQ - University of Sao Paulo  
Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil  
Tel: 55 19 3429 4434  
Fax: 55 19 3429 4285  
Email: ecjorge@esalq.usp.br  
PCR Primers  
BACKWARD: T7.

```

FEATURES      Location/Qualifiers
source        1..612
              /organism="Gallus gallus"
              /mol_type="cDNA"
              /db_type="taxon:9031"
              /db_xref="taxon:9031"
              /cdate="GCE1B1009E03"
              /cissue_type="limb buds"
              /dev_stage="Pool of 3 1/2 days old, 4 1/2 days old and 6
              days old."
              /eubryonic_stage="
              /embryo_bud="

```

/dev/stage= poor\_01\_s72\_c96p8\_Gray...  
days old = embryonic stage"  
/lab host="DH5 alpha"  
/clone lib="LibB Bud - LB1"  
/note=vector: pSPORt1; Site 1: NotI; Site 2: SalI; This  
cDNA library was constructed with the SuperScript Plasmid  
System with Gateway Technology kit (Invitrogen), following a  
manufacturer's protocols. Plasmid DNA was purified using a  
modified alkaline lysis method. Sequencing reactions were  
conducted using the DYANamic ET Dye Terminator sequencing  
kit (Amersham Biosciences) according to the manufacturer's  
recommendations. Clones were sequenced by the 5' end with  
T7 primer.Sequencing reactions were analyzed on MegabACE  
1000 automated DNA sequeencer (Amersham Biosciences). The  
quality and clustering of the BSrs were analyzed using the  
softwares Phred/Cap3/Consed. Only EST sequences with Phred  
quality greater than 20 and at least 200 bp were  
considered for clustering."

[illegible]

ACCESSION	sequence.
VERSION	BU412768
KEYWORDS	BU412768.1 GI:25905439
SOURCE	EST.
ORGANISM	Gallus gallus (chicken)
	Gallus gallus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
	Phasianinae; Gallus.
	1 (bases 1 to 662)
REFERENCE	Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
AUTHORS	Fong, W.T., Wickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
	A Comprehensive Collection of Chicken cDNAs
TITLE	Curr. Biol. 12 (22), 1965-1969 (2002)
JOURNAL	
MEDLINE	22335534
PUBMED	12445392

COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES source  
1. .662  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="layer"  
/db\_xref="taxon:9031"  
/clone="CHEST168b20"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEORBL05"  
/note="Organ: ovary; Vector: pBluescript II KS(+); Site 1:  
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
[Stratagene] vector to accommodate cDNA produced with the  
T-trimmed protocol (Construction of uni-directionally  
cloned cDNA libraries from messenger RNA for improved 3'  
end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
Ligate in double stranded adaptor containing BspI and  
BamHI sites [5'ggcgcgtgcagccgcgacccgaaaaag]  
[5'aattcttttttcggatcggggctgcagc]"

ORIGIN  
Query Match 8.3%; Score 43.4; DB 13; Length 662;  
Best Local Similarity 82.0%; Pred. No. 0.03;  
Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 94 AATCTGCTTAGGTTAGCGTTTGGCTGCTTCGGATGTCAGCGCCAGATATTCGCGT 153  
DB 306 AATATATTAGGATTAGCGTTTGGCTGCTTCGGATGTCAGCGTTAGGTGTGTGT 365  
QY 154 A 154  
DB 366 A 366  
RESULT 74  
BU238874 684 bp mRNA linear EST 26-NOV-2002  
LOCUS 603322034F1 CSEQCHN33 Gallus gallus cDNA clone CHEST249c9 5', mRNA  
DEFINITION sequence.  
ACCESSION BU238874.1 GI:25484934  
VERSION BU238874.1  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 684)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL University of Manchester Institute of Science and Technology  
MEDLINE Curr. Biol. 12 (22), 1965-1969 (2002)  
PUBMED 22335534  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES source  
1. .704  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="layer and broiler"  
/db\_xref="taxon:9031"

COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES source  
1. .684  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST249c9"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN33"  
/note="Organ: liver; Vector: pBluescript II KS(+); Site 1:  
EcoRI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

ORIGIN  
Query Match 8.3%; Score 43.4; DB 13; Length 684;  
Best Local Similarity 82.0%; Pred. No. 0.031;  
Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 94 AATCTGCTTAGGTTAGCGTTTGGCTGCTTCGGATGTCAGCGCCAGATATTCGCGT 153  
DB 361 AATATATTAGGATTAGCGTTTGGCTGCTTCGGATGTCAGCGTTAGGTGTGTGT 420  
QY 154 A 154  
DB 421 A 421  
RESULT 75  
BU476993 704 bp mRNA linear EST 30-NOV-2002  
LOCUS 603845910F1 CSEQRN22 Gallus gallus cDNA clone CHEST834d3 5', mRNA  
DEFINITION sequence.  
ACCESSION BU476993.1 GI:25970570  
VERSION BU476993.1  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 704)  
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL University of Manchester Institute of Science and Technology  
MEDLINE Curr. Biol. 12 (22), 1965-1969 (2002)  
PUBMED 22335534  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES source  
1. .704  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="layer and broiler"  
/db\_xref="taxon:9031"

Fri Mar 12 09:26:03 2004

```

/clone="CHEST834d3"
/sex="Male and female"
/tissue type="Chondrocytes isolated from growth plate
cartilage"
/dev stage="adult"
/lab host="DH10B"
/clone lib="CSQRAN22"
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunted, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."

```

# ORIGIN

```

Query Match      8.3%; Score 43.4; DB 13; Length 704;
Best Local Similarity 82.0%; Pred. No. 0.031;
Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

```

QY 94 AATCTGCTTAGGGTTAGCGCTTTTGGCTGCTTCGGATGTACGGGCGCATATTCGCGT 153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 467 AATATATTATAGGATTAGCGCTTTTGGCTGCTTCGGATGTACGGGCTTAGGTGTGT 526

QY 154 A 154
    |
Db 527 A 527

```

Search completed: March 11, 2004, 11:07:05  
Job time : 3128.7 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:54:28 ; Search time 1476.54 Seconds  
(without alignments)  
7749.596 Million cell updates/sec

Title: US-09-733-368a-1\_COPY\_349\_612  
Perfect score: 264  
Sequence: 1 atgtagcttctgcaatac.....accacatgggtgcaacc 264

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

GenEmbl:  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pin.\*  
35: em.htg.rod.\*  
36: em.htg.man.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	264	100.0	648	6	AX175190 Sequence
2	264	100.0	648	6	AX175195 Sequence
3	262.4	99.4	7086	6	AX743955 Sequence
4	262.4	99.4	8238	6	BD268239 Adenoviru
5	261.4	99.0	330	14	ALRSV4OLTR
6	261.4	99.0	330	14	ALRDCJ
7	261.4	99.0	700	14	REASV4
8	261.4	99.0	1239	14	ALRDA1
9	261.4	99.0	3256	14	ALRDA2
10	261.4	99.0	11572	12	ABI05370
11	261.4	99.0	11627	6	BD261584
12	260.4	98.6	2245	6	AX643582
13	260.4	98.6	6289	12	XXU42373
14	259.2	98.2	5177	6	AX018983
15	259.2	98.2	5177	6	BD136828
16	258.2	97.8	1016	14	REASV3
17	257.6	97.6	4965	6	AR071323
18	257.2	97.4	262	6	AX256413
19	256.4	97.1	562	6	AX643583
20	251.4	95.2	4457	6	AX743954
21	251.4	95.2	7334	6	AX743956
22	248.4	94.1	7286	14	ALVCG
23	248.2	94.0	3557	12	SYNRSV3MV
24	248.2	94.0	4059	6	AR071324
25	248.2	94.0	4341	6	A38214
26	248.2	94.0	4341	6	AX286570
27	248.2	94.0	4839	12	SYNRSV5GPT
28	248.2	94.0	5108	12	SYNRSVNEO
29	248.2	94.0	5564	12	SYNTRC
30	248.2	94.0	5653	6	I56772
31	248.2	94.0	5653	6	I95540
32	248.2	94.0	5736	12	SYNRSVNEO
33	248.2	94.0	6836	6	AR215114
34	248.2	94.0	6836	6	AR302356
35	248.2	94.0	6836	6	AR373228
36	248.2	94.0	6836	6	AR401614
37	248.2	94.0	6836	12	AF346624
38	248.2	94.0	6864	12	XXU19931
39	248.2	94.0	8591	6	I58322
40	248.2	94.0	8591	6	I58323
41	248.2	94.0	8591	6	I60508
42	248.2	94.0	8591	6	I60509
43	248.2	94.0	8591	6	I77052
44	248.2	94.0	8591	6	I77053
45	248.2	94.0	8591	6	I87173
46	248.2	94.0	8591	6	I87174
47	248.2	94.0	9737	6	AR215118
48	248.2	94.0	9737	6	AR215119
49	248.2	94.0	9737	6	AR215124
50	248.2	94.0	9737	6	AR302360
51	248.2	94.0	9737	6	AR302361
52	248.2	94.0	9737	6	AR302366
53	248.2	94.0	9737	6	AR373232
54	248.2	94.0	9737	6	AR373233
55	248.2	94.0	9737	6	AR373238
56	248.2	94.0	9737	6	AR401618
57	248.2	94.0	9737	6	AR401619
58	248.2	94.0	9737	6	AR401624
59	248.2	94.0	9871	6	AR215120
60	248.2	94.0	9871	6	AR302362
61	248.2	94.0	9871	6	AR373234
62	248.2	94.0	9871	6	AR401620
63	248.2	94.0	10060	6	AR215121
64	248.2	94.0	10060	6	AR302363
65	248.2	94.0	10060	6	AR373235